

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Maassab, Hunein F
Herlocher, Martha L

(ii) TITLE OF INVENTION: Cold-adapted Influenza Virus

(iii) NUMBER OF SEQUENCES: 40

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE:** Anna M Lewak
- (B) STREET:** 5445 Corporate Drive
- (C) CITY:** Troy
- (D) STATE:** MI
- (E) COUNTRY:** USA
- (F) ZIP:** 48098

RECEIVED
DEC 03 1993
GROUP 1800

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE:** Floppy disk
- (B) COMPUTER:** IBM PC compatible
- (C) OPERATING SYSTEM:** PC-DOS/MS-DOS
- (D) SOFTWARE:** PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER:** US
- (B) FILING DATE:**
- (C) CLASSIFICATION:**

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME:** Lewak, Anna M
- (B) REGISTRATION NUMBER:** 33006

(C) REFERENCE/DOCKET NUMBER: 2115-00257

01/ (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 313-641-1600

(B) TELEFAX: 313-641-0270

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 890 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Influenza virus

(B) STRAIN: cold-adapted "Master Strain" A/Ann Arbor/6/60 7PI
(H2N2)

(vii) IMMEDIATE SOURCE:

(B) CLONE: NS

(ix) FEATURE:

(A) NAME/KEY: exon

(B) LOCATION: 27..56

(D) OTHER INFORMATION: /product= "nonstructural protein NS2"
/gene= "NS"
/note= "nonstructural protein NS2"
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: conflict

(B) LOCATION: replace(483, "a")

61 (D) OTHER INFORMATION: /note= "a in ca "master" strain and in
wt2(3)"
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: exon

(B) LOCATION: 529..861

(D) OTHER INFORMATION: /product= "nonstructural protein NS2"
/gene= "NS"
/note= "nonstructural protein NS2"
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: conflict

(B) LOCATION: replace(813, "g")

(D) OTHER INFORMATION: /note= "g in ca "master" strain and in
wt2(3)"
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: join(27..56, 529..861)

(D) OTHER INFORMATION: /product= "nonstructural protein NS2"
/gene= "NS"
/note= "nonstructural protein NS2"
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 27..677

(D) OTHER INFORMATION: /product= "nonstructural protein NS1"
/gene= "NS"
/note= "nonstructural protein NS1"
/citation= ([1][2])

(x) PUBLICATION INFORMATION:

Q1 (A) AUTHORS: Herlocher, M L
Maassab, H F
Webster, R G

(B) TITLE: Molecular and biological changes in the cold adapted master strain A/AA/6/60 (H2N2) influenza virus

(C) JOURNAL: Proceedings of the National Academy of Sciences of the USA

(G) DATE: 1993

(K) RELEVANT RESIDUES IN SEQ ID NO:1: FROM 1 TO 890

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Cox, N J
Kitame, F
Kendal, A P
Maassab, H F
Naeye, C

(B) TITLE: Identification of sequence changes in the cold-adapted live attenuated influenza vaccine strain, A/Ann Arbor/6/60(H2N2)

(C) JOURNAL: Virology

(D) VOLUME: 167

(F) PAGES: 554-567

(G) DATE: 1988

(K) RELEVANT RESIDUES IN SEQ ID NO:1: FROM 1 TO 890

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AGCAAAAGCA GGGUGACAAA GACAU	AUG GAU CCU AAC ACU GUG UCA AGC UUU	53
	Met Asp Pro Asn Thr Val Ser Ser Phe	
	1 5	
CAG GUA GAU UGC UUC CUU UGG CAU GUC CGC AAA CAA GUU GCA GAC CAA		101
Gln Val Asp Cys Phe Leu Trp His Val Arg Lys Gln Val Ala Asp Gln		
10 15 20 25		
GAA CUA GGU GAU GCC CCA UUC CUU GAU CGG CUU CGC CGA GAU CAG AAG		149
Glu Leu Gly Asp Ala Pro Phe Leu Asp Arg Leu Arg Arg Asp Gln Lys		
30 35 40		
UCC CUA AGG GGA AGA GGC AGU ACU CUC GGU CUG AAC AUC GAA ACA GCC		197
Ser Leu Arg Gly Arg Gly Ser Thr Leu Gly Leu Asn Ile Glu Thr Ala		
45 50 55		

ACC	CGU	GUU	GGA	AAG	CAG	AUA	GUG	GAG	AGG	AUU	CUG	AAG	GAA	GAA	UCC	245
Thr	Arg	Val	Gly	Lys	Gln	Ile	Val	Glu	Arg	Ile	Leu	Lys	Glu	Glu	Ser	
		60					65					70				
GAU	GAG	GCA	CUU	AAA	AUG	ACC	AUG	GCC	UCC	GCA	CCU	GCU	UCG	CGA	UAC	293
Asp	Glu	Ala	Leu	Lys	Met	Thr	Met	Ala	Ser	Ala	Pro	Ala	Ser	Arg	Tyr	
	75					80					85					
CUA	ACU	GAC	AUG	ACU	AUU	GAG	GAA	AUG	UCA	AGG	GAC	UGG	UUC	AUG	CUA	341
Leu	Thr	Asp	Met	Thr	Ile	Glu	Glu	Met	Ser	Arg	Asp	Trp	Phe	Met	Leu	
	90				95					100					105	
AUG	CCC	AAG	CAG	AAA	GUG	GCA	GGC	CCU	CUU	UGU	AUC	AGA	AUG	GAC	CAG	389
Met	Pro	Lys	Gln	Lys	Val	Ala	Gly	Pro	Leu	Cys	Ile	Arg	Met	Asp	Gln	
				110					115					120		
GCA	AUC	AUG	GAU	AAG	AAC	AUC	AUA	UUG	AAA	GCG	AAU	UUC	AGU	GUG	AUU	437
Ala	Ile	Met	Asp	Lys	Asn	Ile	Ile	Leu	Lys	Ala	Asn	Phe	Ser	Val	Ile	
			125					130					135			
UUU	GAC	CGG	CUA	GAG	ACC	CUA	AUA	UUA	CUA	AGG	GCU	UUC	ACC	GAA	ACG	485
Phe	Asp	Arg	Leu	Glu	Thr	Leu	Ile	Leu	Leu	Arg	Ala	Phe	Thr	Glu	Thr	
		140					145						150			
GGA	GCA	AUU	GUU	GGC	GAA	AUU	UCA	CCA	UUG	CCU	UCU	CUU	CCA	GGA	CAU	533
Gly	Ala	Ile	Val	Gly	Glu	Ile	Ser	Pro	Leu	Pro	Ser	Leu	Pro	Gly	His	
	155					160						165				
ACU	AAU	GAG	GAU	GUC	AAA	AAU	GCA	AUU	GGG	GUC	CUC	AUC	GGA	GGA	CUU	581
Thr	Asn	Glu	Asp	Val	Lys	Asn	Ala	Ile	Gly	Val	Leu	Ile	Gly	Gly	Leu	
	170				175					180					185	
GAA	UGG	AAU	GAU	AAC	ACA	GUU	CGA	GUC	UCU	AAA	ACU	CUA	CAG	AGA	UUC	629
Glu	Trp	Asn	Asp	Asn	Thr	Val	Arg	Val	Ser	Lys	Thr	Leu	Gln	Arg	Phe	
				190					195					200		
GCU	UGG	AGA	AGC	AGU	GAU	GAG	AAU	GGG	AGA	CCU	CCA	CUC	ACU	CCA	AAA	677
Ala	Trp	Arg	Ser	Ser	Asp	Glu	Asn	Gly	Arg	Pro	Pro	Leu	Thr	Pro	Lys	
			205					210					215			
UAGAAACGGA	AAAUGGCGAG	AACAAUUAGG	UCAAAGUUC	GAAGAAAUAA	GAUGGCUGAU											737
UGAAGAAGUG	AGACACAAAU	UGAAGAUAC	AGAGAAUAGU	UUUGAGCAAA	UAACAUUUUAU											797
GCAAGCCUUA	CAGCUGCUAU	UUGAAGUGGA	ACAAGAGAU	AGAACUUUCU	CGUUUCAGCU											857
UAUUUAAUGA	UAAAAACAC	CCUUGUUUCU	ACU													890

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 217 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Asp Pro Asn Thr Val Ser Ser Phe Gln Val Asp Cys Phe Leu Trp
1 5 10 15
His Val Arg Lys Gln Val Ala Asp Gln Glu Leu Gly Asp Ala Pro Phe
20 25 30
Leu Asp Arg Leu Arg Arg Asp Gln Lys Ser Leu Arg Gly Arg Gly Ser
35 40 45
Thr Leu Gly Leu Asn Ile Glu Thr Ala Thr Arg Val Gly Lys Gln Ile
50 55 60
Val Glu Arg Ile Leu Lys Glu Glu Ser Asp Glu Ala Leu Lys Met Thr
65 70 75 80
Met Ala Ser Ala Pro Ala Ser Arg Tyr Leu Thr Asp Met Thr Ile Glu
85 90 95
Glu Met Ser Arg Asp Trp Phe Met Leu Met Pro Lys Gln Lys Val Ala
100 105 110
Gly Pro Leu Cys Ile Arg Met Asp Gln Ala Ile Met Asp Lys Asn Ile
115 120 125
Ile Leu Lys Ala Asn Phe Ser Val Ile Phe Asp Arg Leu Glu Thr Leu
130 135 140
Ile Leu Leu Arg Ala Phe Thr Glu Thr Gly Ala Ile Val Gly Glu Ile
145 150 155 160
Ser Pro Leu Pro Ser Leu Pro Gly His Thr Asn Glu Asp Val Lys Asn
165 170 175
Ala Ile Gly Val Leu Ile Gly Gly Leu Glu Trp Asn Asp Asn Thr Val
180 185 190
Arg Val Ser Lys Thr Leu Gln Arg Phe Ala Trp Arg Ser Ser Asp Glu
195 200 205
Asn Gly Arg Pro Pro Leu Thr Pro Lys
210 215

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 418 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 27..389

(D) OTHER INFORMATION: /product= "Nonstructural protein 2"
/gene= "NS2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AGCAAAAGCA GGGUGACAAA GACAUA AUG GAU CCU AAC ACU GUG UCA AGC UUU	53
Met Asp Pro Asn Thr Val Ser Ser Phe	
1 5	
CAG GAC AUA CUA AUG AGG AUG UCA AAA AUG CAA UUG GGG UCC UCA UCG	101
Gln Asp Ile Leu Met Arg Met Ser Lys Met Gln Leu Gly Ser Ser Ser	
10 15 20 25	
GAG GAC UUG AAU GGA AUG AUA ACA CAG UUC GAG UCU CUA AAA CUC UAC	149
Glu Asp Leu Asn Gly Met Ile Thr Gln Phe Glu Ser Leu Lys Leu Tyr	
30 35 40	
AGA GAU UCG CUU GGA GAA GCA GUG AUG AGA AUG GGA GAC CUC CAC UCA	197
Arg Asp Ser Leu Gly Glu Ala Val Met Arg Met Gly Asp Leu His Ser	
45 50 55	
CUC CAA AAU AGA AAC GGA AAA UGG CGA GAA CAA UUA GGU CAA AAG UUC	245
Leu Gln Asn Arg Asn Gly Lys Trp Arg Glu Gln Leu Gly Gln Lys Phe	
60 65 70	
GAA GAA AUA AGA UGG CUG AUU GAA GAA GUG AGA CAC AAA UUG AAG AUA	293
Glu Glu Ile Arg Trp Leu Ile Glu Glu Val Arg His Lys Leu Lys Ile	
75 80 85	
ACA GAG AAU AGU UUU GAG CAA AUA ACA UUU AUG CAA GCC UUA CAG CUG	341
Thr Glu Asn Ser Phe Glu Gln Ile Thr Phe Met Gln Ala Leu Gln Leu	
90 95 100 105	

CUA UUU GAA GUG GAA CAA GAG AUA AGA ACU UUC UCG UUU CAG CUU AUU 389
 Leu Phe Glu Val Glu Gln Glu Ile Arg Thr Phe Ser Phe Gln Leu Ile
 110 115 120

UAAUGAUAAA AAACACCCUU GUUUCUACU 418

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 121 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Asp Pro Asn Thr Val Ser Ser Phe Gln Asp Ile Leu Met Arg Met
 1 5 10 15
 Ser Lys Met Gln Leu Gly Ser Ser Ser Glu Asp Leu Asn Gly Met Ile
 20 25 30
 Thr Gln Phe Glu Ser Leu Lys Leu Tyr Arg Asp Ser Leu Gly Glu Ala
 35 40 45
 Val Met Arg Met Gly Asp Leu His Ser Leu Gln Asn Arg Asn Gly Lys
 50 55 60
 Trp Arg Glu Gln Leu Gly Gln Lys Phe Glu Glu Ile Arg Trp Leu Ile
 65 70 75 80
 Glu Glu Val Arg His Lys Leu Lys Ile Thr Glu Asn Ser Phe Glu Gln
 85 90 95
 Ile Thr Phe Met Gln Ala Leu Gln Leu Leu Phe Glu Val Glu Gln Glu
 100 105 110
 Ile Arg Thr Phe Ser Phe Gln Leu Ile
 115 120

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1027 base pairs

- 61
- (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Influenza virus
- (B) STRAIN: cold-adapted "Master Strain" A/Ann Arbor/6/60 7PI (H2N2)

(vii) IMMEDIATE SOURCE:

- (B) CLONE: M

(ix) FEATURE:

- (A) NAME/KEY: exon
- (B) LOCATION: 26..51
- (D) OTHER INFORMATION: /product= "matrix protein M2"
/gene= "M"
/note= "matrix protein M2"
/citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: exon
- (B) LOCATION: 740..1004
- (D) OTHER INFORMATION: /product= "matrix protein M2" /gene= "M"
/note= "matrix protein M2"
/citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: conflict
- (B) LOCATION: replace(969, "u")
- (D) OTHER INFORMATION: /note= "u in ca "master" strain and in wt2(3)"
/citation= ([1][2])

(ix) FEATURE:

- a1
- (A) NAME/KEY: CDS
 - (B) LOCATION: join(26..51, 740..1004)
 - (D) OTHER INFORMATION: /product= "matrix protein M2"
/gene= "M"
/note= "matrix protein M2"
/citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 26..781
- (D) OTHER INFORMATION: /product= "matrix protein M1"
/gene= "M"
/note= "matrix protein M1"
/citation= ([1][2])

(x) PUBLICATION INFORMATION:

- (A) AUTHORS: Herlocher, M L
Maassab, H F
Webster, R G
- (B) TITLE: Molecular and biological changes in the cold adapted
master strain A/AA/6/60 (H2N2) influenza virus
- (C) JOURNAL: Proceedings of the National Academy of Sciences of
the USA
- (G) DATE: 1993
- (K) RELEVANT RESIDUES IN SEQ ID NO:5: FROM 1 TO 1027

(x) PUBLICATION INFORMATION:

- (A) AUTHORS: Cox, N J
Kitame, F
Kendal, A P
Maassab, H F
Naeye, C
- (B) TITLE: Identification of sequence changes in the cold-adapted
live attenuated influenza vaccine strain, A/Ann
Arbor/6/60(H2N2)
- (C) JOURNAL: Virology

(D) VOLUME: 167

(F) PAGES: 554-557

(G) DATE: 1988

(K) RELEVANT RESIDUES IN SEQ ID NO:5: FROM 1 TO 1027

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AGCAAAAGCA	GGUAGAUUU	GAAAG	AUG	AGU	CUU	CUA	ACC	GAG	GUC	GAA	ACG		52			
			Met	Ser	Leu	Leu	Thr	Glu	Val	Glu	Thr					
			1				5									
UAC	GUU	CUC	UCU	AUC	AUC	CCG	UCA	GGC	CCC	CUC	AAA	GCC	GAG	AUC	GCA	100
Tyr	Val	Leu	Ser	Ile	Ile	Pro	Ser	Gly	Pro	Leu	Lys	Ala	Glu	Ile	Ala	
10				15					20						25	
CAG	AGA	CUU	GAA	GAU	GUC	UUU	GCU	GGG	AAA	AAC	ACC	GAU	CUU	GAG	GCU	148
Gln	Arg	Leu	Glu	Asp	Val	Phe	Ala	Gly	Lys	Asn	Thr	Asp	Leu	Glu	Ala	
				30				35							40	
CUC	AUG	GAA	UGG	CUA	AAG	ACA	AGA	CCA	AUC	CUG	UCA	CCU	CUG	ACU	AAG	196
Leu	Met	Glu	Trp	Leu	Lys	Thr	Arg	Pro	Ile	Leu	Ser	Pro	Leu	Thr	Lys	
			45					50					55			
GGG	AUU	UUG	GGA	UUU	GUA	UUC	ACG	CUC	ACC	GUG	CCC	AGU	GAG	CGA	GGA	244
Gly	Ile	Leu	Gly	Phe	Val	Phe	Thr	Leu	Thr	Val	Pro	Ser	Glu	Arg	Gly	
		60					65					70				
CUG	CAG	CGU	AGA	CGC	UUU	GUC	CAA	AAU	GCC	CUC	AAU	GGG	AAU	GGG	GAU	292
Leu	Gln	Arg	Arg	Arg	Phe	Val	Gln	Asn	Ala	Leu	Asn	Gly	Asn	Gly	Asp	
	75					80					85					
CCA	AAU	AAC	AUG	GAC	AGA	GCA	GUU	AAA	CUG	UAU	AGA	AAG	CUU	AAG	AGG	340
Pro	Asn	Asn	Met	Asp	Arg	Ala	Val	Lys	Leu	Tyr	Arg	Lys	Leu	Lys	Arg	
90					95				100						105	
GAG	AUA	ACA	UUC	CAU	GGG	GCC	AAA	GAA	AUA	GCG	CUC	AGU	UAU	UCU	GCU	388
Glu	Ile	Thr	Phe	His	Gly	Ala	Lys	Glu	Ile	Ala	Leu	Ser	Tyr	Ser	Ala	
				110				115						120		
GGU	GCA	CUU	GCC	AGU	UGU	AUG	GGC	CUC	AUA	UAC	AAC	AGG	AUG	GGG	GCU	436
Gly	Ala	Leu	Ala	Ser	Cys	Met	Gly	Leu	Ile	Tyr	Asn	Arg	Met	Gly	Ala	
		125					130						135			
GUG	ACC	ACU	GAA	GUG	GUC	UUA	GGC	CUG	GUA	UGU	GCA	ACC	UGU	GAA	CAG	484
Val	Thr	Thr	Glu	Val	Val	Leu	Gly	Leu	Val	Cys	Ala	Thr	Cys	Glu	Gln	
		140				145						150				
AUU	GCU	GAC	UCC	CAG	CAU	AGG	UCU	CAU	AGG	CAA	AUG	GUG	ACA	ACA	ACC	532
Ile	Ala	Asp	Ser	Gln	His	Arg	Ser	His	Arg	Gln	Met	Val	Thr	Thr	Thr	
	155					160					165					

AAU CCA CUA AUA AGA CAU GAG AAC AGA AUG GUU CUG GCC AGC ACU ACA 580
 Asn Pro Leu Ile Arg His Glu Asn Arg Met Val Leu Ala Ser Thr Thr
 170 175 180 185

GCU AAG GCU AUG GAG CAA AUG GCU GGA UCG AGU GAG CAA GCA GCA GAG 628
 Ala Lys Ala Met Glu Gln Met Ala Gly Ser Ser Glu Gln Ala Ala Glu
 190 195 200

GCC AUG GAG GUU GCU AGU CAG GCC AGG CAA AUG GUG CAG GCA AUG AGA 676
 Ala Met Glu Val Ala Ser Gln Ala Arg Gln Met Val Gln Ala Met Arg
 205 210 215

GUU AUU GGG ACU CAU CCU AGC UCC AGU GCU GGU CUA AAA AAU GAU CUU 724
 Val Ile Gly Thr His Pro Ser Ser Ser Ala Gly Leu Lys Asn Asp Leu
 220 225 230

CUU GAA AAU UUG CAG GCC UAU CAG AAA CGA AUG GGG GUG CAG AUG CAA 772
 Leu Glu Asn Leu Gln Ala Tyr Gln Lys Arg Met Gly Val Gln Met Gln
 235 240 245

CGA UUC AAG UGACCCUCUU GUUGUUGCCG CGAGUAUCAU UGGGAUCUUG 821
 Arg Phe Lys
 250

CACUUGAUUAU UGUGGAUUCU UGAUCAUCUU UUUUUCAAAU GCAUUUAUCG CUUCUUUAAA 881

CACGGUCUGA AAAGAGGGCC UUCUACGGAA GGAGUACCAG AGUCUAUGAG GGAAGAAUAU 941

CGAAAGGAAC AGCAGAGUGC UGUGGAUUCU GACGAUAGUC AUUUUGUCAG CAUAGAGCUG 1001

GAGUAAAAAA CUACCUUGUU UCUACU 1027

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 252 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Ser Leu Leu Thr Glu Val Glu Thr Tyr Val Leu Ser Ile Ile Pro
 1 5 10 15

Ser Gly Pro Leu Lys Ala Glu Ile Ala Gln Arg Leu Glu Asp Val Phe
 20 25 30

Ala Gly Lys Asn Thr Asp Leu Glu Ala Leu Met Glu Trp Leu Lys Thr
35 40 45

Arg Pro Ile Leu Ser Pro Leu Thr Lys Gly Ile Leu Gly Phe Val Phe
50 55 60

Thr Leu Thr Val Pro Ser Glu Arg Gly Leu Gln Arg Arg Arg Phe Val
65 70 75 80

Gln Asn Ala Leu Asn Gly Asn Gly Asp Pro Asn Asn Met Asp Arg Ala
85 90 95

Val Lys Leu Tyr Arg Lys Leu Lys Arg Glu Ile Thr Phe His Gly Ala
100 105 110

Lys Glu Ile Ala Leu Ser Tyr Ser Ala Gly Ala Leu Ala Ser Cys Met
115 120 125

Gly Leu Ile Tyr Asn Arg Met Gly Ala Val Thr Thr Glu Val Val Leu
130 135 140

Gly Leu Val Cys Ala Thr Cys Glu Gln Ile Ala Asp Ser Gln His Arg
145 150 155 160

Ser His Arg Gln Met Val Thr Thr Thr Asn Pro Leu Ile Arg His Glu
165 170 175

Asn Arg Met Val Leu Ala Ser Thr Thr Ala Lys Ala Met Glu Gln Met
180 185 190

Ala Gly Ser Ser Glu Gln Ala Ala Glu Ala Met Glu Val Ala Ser Gln
195 200 205

Ala Arg Gln Met Val Gln Ala Met Arg Val Ile Gly Thr His Pro Ser
210 215 220

Ser Ser Ala Gly Leu Lys Asn Asp Leu Leu Glu Asn Leu Gln Ala Tyr
225 230 235 240

Gln Lys Arg Met Gly Val Gln Met Gln Arg Phe Lys
245 250

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 26..316

(D) OTHER INFORMATION: /product= "Matrix M2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AGCAAAAGCA	GGUAGAUUU	GAAAG	AUG	AGU	CUU	CUA	ACC	GAG	GUC	GAA	ACG		52			
			Met	Ser	Leu	Leu	Thr	Glu	Val	Glu	Thr					
			1				5									
CCU	AUC	AGA	AAC	GAA	UGG	GGG	UGC	AGA	UGC	AAC	GAU	UCA	AGU	GAC	CCU	100
Pro	Ile	Arg	Asn	Glu	Trp	Gly	Cys	Arg	Cys	Asn	Asp	Ser	Ser	Asp	Pro	
10				15			20								25	
CUU	GUU	GUU	GCC	GCG	AGU	AUC	AUU	GGG	AUC	UUG	CAC	UUG	AUA	UUG	UGG	148
Leu	Val	Val	Ala	Ala	Ser	Ile	Ile	Gly	Ile	Leu	His	Leu	Ile	Leu	Trp	
			30				35						40			
AUU	CUU	GAU	CAU	CUU	UUU	UUC	AAA	UGC	AUU	UAU	CGC	UUC	UUU	AAA	CAC	196
Ile	Leu	Asp	His	Leu	Phe	Phe	Lys	Cys	Ile	Tyr	Arg	Phe	Phe	Lys	His	
			45				50					55				
GGU	CUG	AAA	AGA	GGG	CCU	UCU	ACG	GAA	GGA	GUA	CCA	GAG	UCU	AUG	AGG	244
Gly	Leu	Lys	Arg	Gly	Pro	Ser	Thr	Glu	Gly	Val	Pro	Glu	Ser	Met	Arg	
		60					65					70				
GAA	GAA	UAU	CGA	AAG	GAA	CAG	CAG	AGU	GCU	GUG	GAU	UCU	GAC	GAU	AGU	292
Glu	Glu	Tyr	Arg	Lys	Glu	Gln	Gln	Ser	Ala	Val	Asp	Ser	Asp	Asp	Ser	
	75				80						85					
CAU	UUU	GUC	AGC	AUA	GAG	CUG	GAG	UAAAAACUA	CCUUGUUUCU	ACU						339
His	Phe	Val	Ser	Ile	Glu	Leu	Glu									
90					95											

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 97 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

Q1
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Ser Leu Leu Thr Glu Val Glu Thr Pro Ile Arg Asn Glu Trp Gly
1 5 10 15
Cys Arg Cys Asn Asp Ser Ser Asp Pro Leu Val Val Ala Ala Ser Ile
20 25 30
Ile Gly Ile Leu His Leu Ile Leu Trp Ile Leu Asp His Leu Phe Phe
35 40 45
Lys Cys Ile Tyr Arg Phe Phe Lys His Gly Leu Lys Arg Gly Pro Ser
50 55 60
Thr Glu Gly Val Pro Glu Ser Met Arg Glu Glu Tyr Arg Lys Glu Gln
65 70 75 80
Gln Ser Ala Val Asp Ser Asp Asp Ser His Phe Val Ser Ile Glu Leu
85 90 95
Glu

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1566 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Influenza virus
- (B) STRAIN: cold-adapted "Master Strain" A/Ann Arbor/6/60 7PI (H2N2)

(vii) IMMEDIATE SOURCE:

- (B) CLONE: NP

a1
(ix) FEATURE:

(A) NAME/KEY: mutation

(B) LOCATION: replace(113, "c")

(D) OTHER INFORMATION: /note= "c in ca "master" strain; a in
wt2(3); a in 1988 reported ca vaccine
strain (manuscript), but c reported in
1988 genbank"
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: conflict

(B) LOCATION: replace(146, "g")

(D) OTHER INFORMATION: /note= "g in ca "master" strain and in
wt2(3)"
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: conflict

(B) LOCATION: replace(627, "c")

(D) OTHER INFORMATION: /note= "c in ca "master" strain and in
wt2(3); a in 1988 reported ca vaccine
strain"
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: conflict

(B) LOCATION: replace(909, "g")

(D) OTHER INFORMATION: /note= "g in ca "master" strain and in
wt2(3); c in 1988 reported ca vaccine
strain"
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: conflict

(B) LOCATION: replace(1550, "a")

(D) OTHER INFORMATION: /note= "a in ca "master" strain and in
wt2(3)"

/citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 46..1539
- (D) OTHER INFORMATION: /product= "Nucleoprotein"
/gene= "NP"
/note= "nucleoprotein"
/citation= ([1][2])

(x) PUBLICATION INFORMATION:

- (A) AUTHORS: Herlocher, M L
Maassab, H F
Webster, R W
- (B) TITLE: Molecular and biological changes in the cold adapted
master strain A/AA/6/60 (H2N2) influenza virus
- (C) JOURNAL: Proceedings of the National Academy of Sciences of
the USA
- (G) DATE: 1993
- (K) RELEVANT RESIDUES IN SEQ ID NO:9: FROM 1 TO 1566

(x) PUBLICATION INFORMATION:

- (A) AUTHORS: Cox, N J
Kitame, F
Kendal, A P
Maassab, H F
Naeve, C
- (B) TITLE: Identification of sequence changes in the cold-adapted
live attenuated influenza vaccine strain, A/Ann
Arbor/6/60 (H2N2)
- (C) JOURNAL: Virology
- (D) VOLUME: 167
- (F) PAGES: 554-567
- (G) DATE: 1988
- (K) RELEVANT RESIDUES IN SEQ ID NO:9: FROM 1 TO 1566

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

AGCAAAAGCA GGGUAGAUAA UCACUCACUG AGUGACAUCA AAAUC AUG GCG UCC 54
Met Ala Ser
1

CAA GGC ACC AAA CGG UCU UAU GAA CAG AUG GAA ACU GAU GGG GAA CGC 102
Gln Gly Thr Lys Arg Ser Tyr Glu Gln Met Glu Thr Asp Gly Glu Arg
5 10 15

CAG AAU GCA ACU GAA AUC AGA GCA UCC GUC GGG AAG AUG AUU GGU GGA 150
Gln Asn Ala Thr Glu Ile Arg Ala Ser Val Gly Lys Met Ile Gly Gly
20 25 30 35

AUU GGA CGA UUC UAC AUC CAA AUG UGC ACC GAA CUU AAA CUC AGU GAU 198
Ile Gly Arg Phe Tyr Ile Gln Met Cys Thr Glu Leu Lys Leu Ser Asp
40 45 50

UAU GAG GGG CGG CUG AUC CAG AAC AGC UUA ACA AUA GAG AGA AUG GUG 246
Tyr Glu Gly Arg Leu Ile Gln Asn Ser Leu Thr Ile Glu Arg Met Val
55 60 65

CUC UCU GCU UUU GAC GAG AGG AGG AAU AAA UAU CUG GAA GAA CAU CCC 294
Leu Ser Ala Phe Asp Glu Arg Arg Asn Lys Tyr Leu Glu Glu His Pro
70 75 80

AGC GCG GGG AAG GAU CCU AAG AAA ACU GGA GGA CCC AUA UAC AAG AGA 342
Ser Ala Gly Lys Asp Pro Lys Lys Thr Gly Gly Pro Ile Tyr Lys Arg
85 90 95

GUA GAU GGA AAG UGG AUG AGG GAA CUC GUC CUU UAU GAC AAA GAA GAA 390
Val Asp Gly Lys Trp Met Arg Glu Leu Val Leu Tyr Asp Lys Glu Glu
100 105 110 115

AUA AGG CGA AUC UGG CGC CAA GCU AAU AAU GGU GAU GAU GCA ACA GCU 438
Ile Arg Arg Ile Trp Arg Gln Ala Asn Asn Gly Asp Asp Ala Thr Ala
120 125 130

GGU CUG ACU CAC AUG AUG AUC UGG CAU UCC AAU UUG AAU GAU ACA ACA 486
Gly Leu Thr His Met Met Ile Trp His Ser Asn Leu Asn Asp Thr Thr
135 140 145

UAC CAG AGG ACA AGA GCU CUU GUU CGC ACC GGA AUG GAU CCC AGG AUG 534
Tyr Gln Arg Thr Arg Ala Leu Val Arg Thr Gly Met Asp Pro Arg Met
150 155 160

UGC UCU UUG AUG CAG GGU UCG ACU CUC CCU AGG AGG UCU GGA GCC GCA 582
Cys Ser Leu Met Gln Gly Ser Thr Leu Pro Arg Arg Ser Gly Ala Ala
165 170 175

GGC GCU GCA GUC AAA GGA GUU GGG ACA AUG GUG AUG GAG UUG AUC AGG 630
Gly Ala Ala Val Lys Gly Val Gly Thr Met Val Met Glu Leu Ile Arg
180 185 190 195

AUG Met	AUC Ile	AAA Lys	CGU Arg	GGG Gly 200	AUC Ile	AAU Asn	GAU Asp	CGG Arg	AAC Asn 205	UUC Phe	UGG Trp	AGA Arg	GGU Gly	GAG Glu 210	AAU Asn	678
GGG Gly	CGG Arg	AAA Lys	ACA Thr 215	AGG Arg	AAU Asn	GCU Ala	UAU Tyr	GAG Glu 220	AGA Arg	AUG Met	UGC Cys	AAC Asn	AUU Ile 225	CUC Leu	AAA Lys	726
GGA Gly	AAA Lys	UUU Phe 230	CAA Gln	ACA Thr	GCU Ala	GCA Ala	CAA Gln 235	AGA Arg	GCA Ala	AUG Met	AUG Met	GAU Asp 240	CAA Gln	GUG Val	AGA Arg	774
GAA Glu	AGC Ser 245	CGG Arg	AAC Asn	CCA Pro	GGA Gly	AAU Asn 250	GCU Ala	GAG Glu	AUC Ile	GAA Glu	GAU Asp 255	CUC Leu	AUC Ile	UUU Phe	CUG Leu	822
GCA Ala 260	CGG Arg	UCU Ser	GCA Ala	CUC Leu	AUA Ile 265	UUG Leu	AGA Arg	GGG Gly	UCA Ser	GUU Val 270	GCU Ala	CAC His	AAA Lys	UCU Ser	UGU Cys 275	870
CUG Leu	CCU Pro	GCC Ala	UGU Cys	GUG Val 280	UAU Tyr	GGA Gly	CCU Pro	GCC Ala	GUA Val 285	GCC Ala	AGU Ser	GGG Gly	UAC Tyr	GAC Asp 290	UUC Phe	918
GAA Glu	AAA Lys	GAG Glu	GGA Gly 295	UAC Tyr	UCU Ser	UUA Leu	GUA Val	GGG Gly 300	AUA Ile	GAC Asp	CCU Pro	UUC Phe	AAA Lys 305	CUG Leu	CUU Leu	966
CAA Gln	AAC Asn	AGC Ser 310	CAA Gln	GUA Val	UAC Tyr	AGC Ser	CUA Leu 315	AUC Ile	AGA Arg	CCG Pro	AAU Asn	GAG Glu 320	AAU Asn	CCA Pro	GCA Ala	1014
CAC His	AAG Lys 325	AGU Ser	CAG Gln	CUG Leu	GUG Val	UGG Trp 330	AUG Met	GCA Ala	UGC Cys	AAU Asn	UCU Ser 335	GCU Ala	GCA Ala	UUU Phe	GAA Glu	1062
GAU Asp 340	CUA Leu	AGA Arg	GUA Val	UCA Ser	AGC Ser 345	UUC Phe	AUC Ile	AGA Arg	GGG Gly	ACC Thr 350	AAA Lys	GUA Val	AUC Ile	CCA Pro	AGG Arg 355	1110
GGG Gly	AAA Lys	CUU Leu	UCC Ser	ACU Thr 360	AGA Arg	GGA Gly	GUA Val	CAA Gln	AUU Ile 365	GCU Ala	UCA Ser	AAU Asn	GAA Glu	AAC Asn 370	AUG Met	1158
GAU Asp	ACU Thr	AUG Met	GGA Gly 375	UCA Ser	AGU Ser	ACU Thr	CUU Leu	GAA Glu 380	CUG Leu	AGA Arg	AGC Ser	AGG Arg	UAC Tyr	UGG Trp	GCC Ala	1206
AUA Ile	AGG Arg	ACC Thr 390	AGA Arg	AGU Ser	GGA Gly	GGA Gly	AAC Asn 395	ACU Thr	AAU Asn	CAA Gln	CAG Gln	AGG Arg 400	GCC Ala	UCU Ser	GCA Ala	1254
GGU Gly	CAA Gln 405	AUC Ile	AGU Ser	GUA Val	CAA Gln	CCU Pro	ACG Thr	UUU Phe	UCU Ser	GUG Val	CAA Gln 415	AGA Arg	AAC Asn	CUC Leu	CCA Pro	1302

UUU GAC AAA CCA ACC AUC AUG GCA GCA UUC ACU GGG AAU GCA GAG GGA 1350
Phe Asp Lys Pro Thr Ile Met Ala Ala Phe Thr Gly Asn Ala Glu Gly
420 425 430 435

AGA ACA UCA GAC AUG AGG GCA GAA AUC AUA AGG AUG AUG GAA GGU GCA 1398
Arg Thr Ser Asp Met Arg Ala Glu Ile Ile Arg Met Met Glu Gly Ala
440 445 450

AAA CCA GAA GAA GUG UCC UUC CAG GGG CGG GGA GUC UUC GAG CUC UCG 1446
Lys Pro Glu Glu Val Ser Phe Gln Gly Arg Gly Val Phe Glu Leu Ser
455 460 465

GAC GAA AAG GCA ACG AAC CCG AUC GUG CCC UCU UUU GAC AUG AGU AAU 1494
Asp Glu Lys Ala Thr Asn Pro Ile Val Pro Ser Phe Asp Met Ser Asn
470 475 480

GAA GGA UCU UAU UUC UUC GGA GAC AAU GCA GAG GAG UAC GAC AAU 1539
Glu Gly Ser Tyr Phe Phe Gly Asp Asn Ala Glu Glu Tyr Asp Asn
485 490 495

UAAGGAAAAA AUACCCUUGU UUCUACU 1566

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 498 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Ala Ser Gln Gly Thr Lys Arg Ser Tyr Glu Gln Met Glu Thr Asp
1 5 10 15

Gly Glu Arg Gln Asn Ala Thr Glu Ile Arg Ala Ser Val Gly Lys Met
20 25 30

Ile Gly Gly Ile Gly Arg Phe Tyr Ile Gln Met Cys Thr Glu Leu Lys
35 40 45

Leu Ser Asp Tyr Glu Gly Arg Leu Ile Gln Asn Ser Leu Thr Ile Glu
50 55 60

Arg Met Val Leu Ser Ala Phe Asp Glu Arg Arg Asn Lys Tyr Leu Glu
65 70 75 80

Glu His Pro Ser Ala Gly Lys Asp Pro Lys Lys Thr Gly Gly Pro Ile

85 90 95
 Tyr Lys Arg Val Asp Gly Lys Trp Met Arg Glu Leu Val Leu Tyr Asp
 100 105 110
 Lys Glu Glu Ile Arg Arg Ile Trp Arg Gln Ala Asn Asn Gly Asp Asp
 115 120 125
 Ala Thr Ala Gly Leu Thr His Met Met Ile Trp His Ser Asn Leu Asn
 130 135 140
 Asp Thr Thr Tyr Gln Arg Thr Arg Ala Leu Val Arg Thr Gly Met Asp
 145 150 155 160
 Pro Arg Met Cys Ser Leu Met Gln Gly Ser Thr Leu Pro Arg Arg Ser
 165 170 175
 Gly Ala Ala Gly Ala Ala Val Lys Gly Val Gly Thr Met Val Met Glu
 180 185 190
 Leu Ile Arg Met Ile Lys Arg Gly Ile Asn Asp Arg Asn Phe Trp Arg
 195 200 205
 Gly Glu Asn Gly Arg Lys Thr Arg Asn Ala Tyr Glu Arg Met Cys Asn
 210 215 220
 Ile Leu Lys Gly Lys Phe Gln Thr Ala Ala Gln Arg Ala Met Met Asp
 225 230 235 240
 Gln Val Arg Glu Ser Arg Asn Pro Gly Asn Ala Glu Ile Glu Asp Leu
 245 250 255
 Ile Phe Leu Ala Arg Ser Ala Leu Ile Leu Arg Gly Ser Val Ala His
 260 265 270
 Lys Ser Cys Leu Pro Ala Cys Val Tyr Gly Pro Ala Val Ala Ser Gly
 275 280 285
 Tyr Asp Phe Glu Lys Glu Gly Tyr Ser Leu Val Gly Ile Asp Pro Phe
 290 295 300
 Lys Leu Leu Gln Asn Ser Gln Val Tyr Ser Leu Ile Arg Pro Asn Glu
 305 310 315 320
 Asn Pro Ala His Lys Ser Gln Leu Val Trp Met Ala Cys Asn Ser Ala
 325 330 335
 Ala Phe Glu Asp Leu Arg Val Ser Ser Phe Ile Arg Gly Thr Lys Val
 340 345 350
 Ile Pro Arg Gly Lys Leu Ser Thr Arg Gly Val Gln Ile Ala Ser Asn
 355 360 365
 Glu Asn Met Asp Thr Met Gly Ser Ser Thr Leu Glu Leu Arg Ser Arg
 370 375 380

Tyr Trp Ala Ile Arg Thr Arg Ser Gly Gly Asn Thr Asn Gln Gln Arg
 385 390 395 400
 Ala Ser Ala Gly Gln Ile Ser Val Gln Pro Thr Phe Ser Val Gln Arg
 405 410 415
 Asn Leu Pro Phe Asp Lys Pro Thr Ile Met Ala Ala Phe Thr Gly Asn
 420 425 430
 Ala Glu Gly Arg Thr Ser Asp Met Arg Ala Glu Ile Ile Arg Met Met
 435 440 445
 Glu Gly Ala Lys Pro Glu Glu Val Ser Phe Gln Gly Arg Gly Val Phe
 450 455 460
 Glu Leu Ser Asp Glu Lys Ala Thr Asn Pro Ile Val Pro Ser Phe Asp
 465 470 475 480
 Met Ser Asn Glu Gly Ser Tyr Phe Phe Gly Asp Asn Ala Glu Glu Tyr
 485 490 495

Asp Asn

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2233 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Influenza virus
- (B) STRAIN: cold-adapted "Master Strain" A/Ann Arbor/6/60 7PI (H2N2)

(vii) IMMEDIATE SOURCE:

- (B) CLONE: PA

(ix) FEATURE:

- (A) NAME/KEY: conflict

a'
(B) LOCATION: replace(20, "c")

(D) OTHER INFORMATION: /note= "c in ca "master" strain and in
wt2(3)"
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: conflict

(B) LOCATION: replace(75, "g")

(D) OTHER INFORMATION: /note= "g in ca "master" strain and in
wt2(3); u in 1988 reported ca vaccine
strain"
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: conflict

(B) LOCATION: replace(1861, "g")

(D) OTHER INFORMATION: /note= "g in ca "master" strain and in
wt2(3)"
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: conflict

(B) LOCATION: replace(2167..2168, "cc")

(D) OTHER INFORMATION: /note= "cc in ca "master" strain and in
wt2(3)"
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 25..2172

(D) OTHER INFORMATION: /product= "polymerase acidic protein"
/gene= "PA"
/note= "polymerase acidic protein"
/citation= ([1][2])

(x) PUBLICATION INFORMATION:

- (A) AUTHORS: Herlocher, M L
Maassab, H F
Webster, R G
- (B) TITLE: Molecular and biological changes in the cold adapted master strain A/AA/6/60 (H2N2) influenza virus
- (C) JOURNAL: Proceedings of the National Academy of Sciences of the USA
- (G) DATE: 1993
- (K) RELEVANT RESIDUES IN SEQ ID NO:11: FROM 1 TO 2233

(x) PUBLICATION INFORMATION:

- (A) AUTHORS: Cox, N J
Kitame, F
Kendal, A P
Maassab, H F
Naeve, C
- (B) TITLE: Identification of sequence changes in the cold-adapted live attenuated influenza strain, A/Ann Arbor/6/60(H2N2)
- (C) JOURNAL: Virology
- (D) VOLUME: 167
- (F) PAGES: 554-567
- (G) DATE: 1988
- (K) RELEVANT RESIDUES IN SEQ ID NO:11: FROM 1 TO 2233

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AGCGAAAGCA GGUACUGAUC CGAA AUG GAA GAU UUU GUG CGA CAA UGC UUC	51
Met Glu Asp Phe Val Arg Gln Cys Phe	
1 5	
AAU CCG AUG AUU GUC GAG CUU GCG GAA AAA GCA AUG AAA GAG UAU GGA	99
Asn Pro Met Ile Val Glu Leu Ala Glu Lys Ala Met Lys Glu Tyr Gly	
10 15 20 25	
GAG GAU CUG AAA AUC GAA ACA AAC AAA UUU GCA GCA AUA UGC ACU CAC	147
Glu Asp Leu Lys Ile Glu Thr Asn Lys Phe Ala Ala Ile Cys Thr His	
30 35 40	
UUG GAA GUA UGC UUC AUG UAU UCA GAU UUU CAU UUC AUC AAU GAG CAA	195
Leu Glu Val Cys Phe Met Tyr Ser Asp Phe His Phe Ile Asn Glu Gln	
45 50 55	

GGC Gly	GAG Glu	UCA Ser 60	AUA Ile	AUA Ile	GUA Val	GAG Glu	CUU Leu 65	GAU Asp	GAU Asp	CCA Pro	AAU Asn	GCA Ala 70	CUU Leu	UUG Leu	AAG Lys	243
CAC His	AGA Arg 75	UUU Phe	GAA Glu	AUA Ile	AUA Ile	GAG Glu 80	GGA Gly	AGA Arg	GAU Asp	CGC Arg	ACA Thr 85	AUG Met	GCC Ala	UGG Trp	ACA Thr	291
GUA Val 90	GUA Val	AAC Asn	AGU Ser	AUU Ile	UGC Cys 95	AAC Asn	ACU Thr	ACA Thr	GGA Gly	GCU Ala 100	GAG Glu	AAA Lys	CCG Pro	AAG Lys	UUU Phe 105	339
CUG Leu	CCA Pro	GAU Asp	UUG Leu	UAU Tyr 110	GAU Asp	UAC Tyr	AAG Lys	GAG Glu	AAU Asn 115	AGA Arg	UUC Phe	AUC Ile	GAG Glu	AUU Ile 120	GGA Gly	387
GUG Val	ACA Thr	AGG Arg 125	AGG Arg	GAA Glu	GUC Val	CAC His	AUA Ile	UAC Tyr 130	UAU Tyr	CUU Leu	GAA Glu	AAG Lys	GCC Ala 135	AAU Asn	AAA Lys	435
AUU Ile	AAA Lys	UCU Ser 140	GAG Glu	AAG Lys	ACA Thr	CAC His	AUC Ile 145	CAC His	AUU Ile	UUC Phe	UCA Ser	UUC Phe 150	ACU Thr	GGG Gly	GAA Glu	483
GAA Glu 155	AUG Met	GCC Ala	ACA Thr	AAG Lys	GCC Ala	GAC Asp 160	UAC Tyr	ACU Thr	CUC Leu	GAU Asp 165	GAG Glu 165	GAA Glu	AGC Ser	AGG Arg	GCU Ala	531
AGG Arg 170	AUC Ile	AAA Lys	ACC Thr	AGA Arg	CUA Leu 175	UUC Phe	ACC Thr	AUA Ile	AGA Arg	CAA Gln 180	GAA Glu	AUG Met	GCU Ala	AGC Ser	AGA Arg 185	579
GGC Gly	CUC Leu	UGG Trp	GAU Asp 190	UCC Ser	UUU Phe	CAU His	CAG Gln	UCC Ser	GAA Glu 195	AGA Arg	GGC Gly	GAA Glu	GAA Glu 200	ACA Thr	AUU Ile	627
GAA Glu	GAA Glu	AGA Arg 205	UUU Phe	GAA Glu	AUC Ile	ACA Thr	GGG Gly 210	ACA Thr	AUG Met	CGC Arg	AGG Arg	CUC Leu	GCC Ala 215	GAC Asp	CAA Gln	675
AGU Ser	CUC Leu	CCG Pro 220	CCG Pro	AAC Asn	UUC Phe	UCC Ser	UGC Cys 225	CUU Leu	GAG Glu	AAU Asn	UUU Phe	AGA Arg 230	GCC Ala	UAU Tyr	GUG Val	723
GAU Asp 235	GGA Gly	UUC Phe	GAA Glu	CCG Pro	AAC Asn	GGC Gly 240	UAC Tyr	AUU Ile	GAG Glu	GGC Gly	AAG Lys 245	CUU Leu	UCU Ser	CAA Gln	AUG Met	771
UCC Ser 250	AAA Lys	GAA Glu	GUA Val	AAU Asn	GCU Ala 255	AAA Lys	AUU Ile	GAA Glu	CCU Pro	UUU Phe 260	CUG Leu	AAA Lys	ACA Thr	ACA Thr	CCA Pro 265	819
AGA Arg	CCA Pro	AUU Ile	AGA Arg	CUU Leu 270	CCG Pro	GAU Asp	GGG Gly	CCU Pro	CCU Pro 275	UGU Cys	UCU Ser	CAG Gln	CGG Arg	UCC Ser 280	AAA Lys	867

UUC Phe	CUG Leu	CUG Leu	AUG Met 285	GAU Asp	GCU Ala	UUA Leu	AAA Lys	UUA Leu 290	AGC Ser	AUU Ile	GAG Glu	GAC Asp 295	CCA Pro	AGU Ser	CAC His	915
GAA Glu	GGA Gly	GAG Glu 300	GGA Gly	AUA Ile	CCA Pro	CUA Leu	UAU Tyr 305	GAU Asp	GCG Ala	AUC Ile	AAG Lys	UGU Cys 310	AUG Met	AGA Arg	ACA Thr	963
UUC Phe 315	UUU Phe	GGA Gly	UGG Trp	AAA Lys	GAA Glu	CCC Pro 320	UAU Tyr	GUU Val	GUU Val	AAA Lys	CCA Pro 325	CAC His	GAA Glu	AAG Lys	GGA Gly	1011
AUA Ile 330	AAU Asn	CCA Pro	AAU Asn	UAU Tyr	CUG Leu 335	CUG Leu	UCA Ser	UGG Trp	AAG Lys	CAA Gln 340	GUA Val	CUG Leu	GCA Ala	GAA Glu	CUG Leu 345	1059
CAG Gln	GAC Asp	AUU Ile	GAG Glu	AAU Asn 350	GAG Glu	GAG Glu	AAG Lys	AUU Ile	CCA Pro 355	AGA Arg	ACC Thr	AAA Lys	AAC Asn	AUG Met 360	AAG Lys	1107
AAA Lys	ACG Thr	AGU Ser	CAG Gln 365	CUA Leu	AAG Lys	UGG Trp	GCA Ala	CUU Leu 370	GGU Gly	GAG Glu	AAC Asn	AUG Met	GCA Ala 375	CCA Pro	GAG Glu	1155
AAG Lys	GUA Val	GAC Asp 380	UUU Phe	GAC Asp	GAC Asp	UGU Cys	AGA Arg 385	GAU Asp	GUA Val	AGC Ser	GAU Asp	UUG Leu 390	AAG Lys	CAA Gln	UAU Tyr	1203
GAU Asp 395	AGU Ser	GAU Asp	GAA Glu	CCU Pro	GAA Glu	UUA Leu 400	AGG Arg	UCA Ser	CUU Leu	UCA Ser	AGC Ser 405	UGG Trp	AUC Ile	CAG Gln	AAU Asn	1251
GAG Glu 410	UUC Phe	AAC Asn	AAG Lys	GCA Ala	UGC Cys 415	GAG Glu	CUG Leu	ACC Thr	GAU Asp	UCA Ser 420	AUC Ile	UGG Trp	AUA Ile	GAG Glu	CUC Leu 425	1299
GAU Asp	GAG Glu	AUU Ile	GGA Gly	GAA Glu 430	GAU Asp	GUG Val	GCU Ala	CCA Pro	AUU Ile 435	GAA Glu	CAC His	AUU Ile	GCA Ala	AGC Ser 440	AUG Met	1347
AGA Arg	AGG Arg	AAU Asn	UAC Tyr 445	UUC Phe	ACA Thr	GCA Ala	GAG Glu	GUG Val 450	UCU Ser	CAU His	UGC Cys	AGA Arg	GCC Ala 455	ACA Thr	GAA Glu	1395
UAU Tyr	AUA Ile	AUG Met 460	AAG Lys	GGG Gly	GUA Val	UAC Tyr	AUU Ile 465	AAU Asn	ACU Thr	GCC Ala	UUG Leu	CUU Leu 470	AAU Asn	GCA Ala	UCC Ser	1443
UGU Cys	GCA Ala 475	GCA Ala	AUG Met	GAC Asp	GAU Asp	UUC Phe 480	CAA Gln	CUA Leu	AUU Ile	CCC Pro	AUG Met 485	AUA Ile	AGC Ser	AAA Lys	UGU Cys	1491
AGA Arg 490	ACU Thr	AAA Lys	GAG Glu	GGA Gly	AGG Arg 495	CGA Arg	AAG Lys	ACC Thr	AAU Asn	UUA Leu 500	UAU Tyr	GGU Gly	UUC Phe	AUC Ile	AUA Ile 505	1539

[illegible]

AAAAAGUACC UUGUUUCUAC U

2233

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 716 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met	Glu	Asp	Phe	Val	Arg	Gln	Cys	Phe	Asn	Pro	Met	Ile	Val	Glu	Leu	1	5	10	15
Ala	Glu	Lys	Ala	Met	Lys	Glu	Tyr	Gly	Glu	Asp	Leu	Lys	Ile	Glu	Thr	20	25	30	
Asn	Lys	Phe	Ala	Ala	Ile	Cys	Thr	His	Leu	Glu	Val	Cys	Phe	Met	Tyr	35	40	45	
Ser	Asp	Phe	His	Phe	Ile	Asn	Glu	Gln	Gly	Glu	Ser	Ile	Ile	Val	Glu	50	55	60	
Leu	Asp	Asp	Pro	Asn	Ala	Leu	Leu	Lys	His	Arg	Phe	Glu	Ile	Ile	Glu	65	70	75	80
Gly	Arg	Asp	Arg	Thr	Met	Ala	Trp	Thr	Val	Val	Asn	Ser	Ile	Cys	Asn	85	90	95	
Thr	Thr	Gly	Ala	Glu	Lys	Pro	Lys	Phe	Leu	Pro	Asp	Leu	Tyr	Asp	Tyr	100	105	110	
Lys	Glu	Asn	Arg	Phe	Ile	Glu	Ile	Gly	Val	Thr	Arg	Arg	Glu	Val	His	115	120	125	
Ile	Tyr	Tyr	Leu	Glu	Lys	Ala	Asn	Lys	Ile	Lys	Ser	Glu	Lys	Thr	His	130	135	140	
Ile	His	Ile	Phe	Ser	Phe	Thr	Gly	Glu	Glu	Met	Ala	Thr	Lys	Ala	Asp	145	150	155	160
Tyr	Thr	Leu	Asp	Glu	Glu	Ser	Arg	Ala	Arg	Ile	Lys	Thr	Arg	Leu	Phe	165	170	175	
Thr	Ile	Arg	Gln	Glu	Met	Ala	Ser	Arg	Gly	Leu	Trp	Asp	Ser	Phe	His	180	185	190	

Gln Ser Glu Arg Gly Glu Glu Thr Ile Glu Glu Arg Phe Glu Ile Thr
 195 200 205
 Gly Thr Met Arg Arg Leu Ala Asp Gln Ser Leu Pro Pro Asn Phe Ser
 210 215 220
 Cys Leu Glu Asn Phe Arg Ala Tyr Val Asp Gly Phe Glu Pro Asn Gly
 225 230 235 240
 Tyr Ile Glu Gly Lys Leu Ser Gln Met Ser Lys Glu Val Asn Ala Lys
 245 250 255
 Ile Glu Pro Phe Leu Lys Thr Thr Pro Arg Pro Ile Arg Leu Pro Asp
 260 265 270
 Gly Pro Pro Cys Ser Gln Arg Ser Lys Phe Leu Leu Met Asp Ala Leu
 275 280 285
 Lys Leu Ser Ile Glu Asp Pro Ser His Glu Gly Glu Gly Ile Pro Leu
 290 295 300
 Tyr Asp Ala Ile Lys Cys Met Arg Thr Phe Phe Gly Trp Lys Glu Pro
 305 310 315 320
 Tyr Val Val Lys Pro His Glu Lys Gly Ile Asn Pro Asn Tyr Leu Leu
 325 330 335
 Ser Trp Lys Gln Val Leu Ala Glu Leu Gln Asp Ile Glu Asn Glu Glu
 340 345 350
 Lys Ile Pro Arg Thr Lys Asn Met Lys Lys Thr Ser Gln Leu Lys Trp
 355 360 365
 Ala Leu Gly Glu Asn Met Ala Pro Glu Lys Val Asp Phe Asp Asp Cys
 370 375 380
 Arg Asp Val Ser Asp Leu Lys Gln Tyr Asp Ser Asp Glu Pro Glu Leu
 385 390 395 400
 Arg Ser Leu Ser Ser Trp Ile Gln Asn Glu Phe Asn Lys Ala Cys Glu
 405 410 415
 Leu Thr Asp Ser Ile Trp Ile Glu Leu Asp Glu Ile Gly Glu Asp Val
 420 425 430
 Ala Pro Ile Glu His Ile Ala Ser Met Arg Arg Asn Tyr Phe Thr Ala
 435 440 445
 Glu Val Ser His Cys Arg Ala Thr Glu Tyr Ile Met Lys Gly Val Tyr
 450 455 460
 Ile Asn Thr Ala Leu Leu Asn Ala Ser Cys Ala Ala Met Asp Asp Phe
 465 470 475 480
 Gln Leu Ile Pro Met Ile Ser Lys Cys Arg Thr Lys Glu Gly Arg Arg

485 490 495
 Lys Thr Asn Leu Tyr Gly Phe Ile Ile Lys Gly Arg Ser His Leu Arg
 500 505 510
 Asn Asp Thr Asp Val Val Asn Phe Val Ser Met Glu Phe Ser Leu Thr
 515 520 525
 Asp Pro Arg Leu Glu Pro His Lys Trp Glu Lys Tyr Cys Val Leu Glu
 530 535 540
 Ile Gly Asp Met Leu Leu Arg Ser Ala Ile Gly Gln Val Ser Arg Pro
 545 550 555 560
 Met Phe Leu Tyr Val Arg Thr Asn Gly Thr Ser Lys Ile Lys Met Lys
 565 570 575
 Trp Gly Met Glu Met Arg Arg Cys Leu Leu Gln Ser Leu Gln Gln Ile
 580 585 590
 Glu Ser Met Ile Glu Ala Glu Ser Ser Val Lys Glu Lys Asp Met Thr
 595 600 605
 Lys Glu Phe Phe Glu Asn Lys Ser Glu Thr Trp Pro Ile Gly Glu Ser
 610 615 620
 Pro Lys Gly Val Glu Glu Gly Ser Ile Gly Lys Val Cys Arg Thr Leu
 625 630 635 640
 Leu Ala Lys Ser Val Phe Asn Ser Leu Tyr Ala Ser Pro Gln Leu Glu
 645 650 655
 Gly Phe Ser Ala Glu Ser Arg Lys Leu Leu Leu Val Val Gln Ala Leu
 660 665 670
 Arg Asp Asn Leu Glu Pro Gly Thr Phe Asp Leu Gly Gly Leu Tyr Glu
 675 680 685
 Ala Ile Glu Glu Cys Leu Ile Asn Asp Pro Trp Val Leu Leu Asn Ala
 690 695 700
 Ser Trp Phe Asn Ser Phe Leu Thr His Ala Pro Arg
 705 710 715

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2341 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

61
(ii) MOLECULE TYPE: RNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Influenza virus

(B) STRAIN: cold adapted "Master Strain" A/AA/6/60 7PI (H2N2)

(vii) IMMEDIATE SOURCE:

(B) CLONE: PB1

(ix) FEATURE:

(A) NAME/KEY: conflict

(B) LOCATION: replace(123, "g")

(D) OTHER INFORMATION: /note= "g in ca "master" strain and in
wt2(3)"
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: conflict

(B) LOCATION: replace(486, "u")

(D) OTHER INFORMATION: /note= "u in ca "master" strain and in
wt2(3)"
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: conflict

(B) LOCATION: replace(1195, "g")

(D) OTHER INFORMATION: /note= "g in ca "master" strain and in
wt2(3)"
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: mutation

(B) LOCATION: replace(1276, "g")

a1
(D) OTHER INFORMATION: /note= "g in ca "master" strain; a in
wt2(3); g in 1988 reported ca vaccine
strain"
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: conflict

(B) LOCATION: replace(1395, "u")

(D) OTHER INFORMATION: /note= "u in ca "master" strain and in
wt2(3)"
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: conflict

(B) LOCATION: replace(1766, "g")

(D) OTHER INFORMATION: /note= "g in ca "master" strain and in
wt2(3)"
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: conflict

(B) LOCATION: replace(2005, "a")

(D) OTHER INFORMATION: /note= "a in ca "master" strain and in
wt2(3)"
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: conflict

(B) LOCATION: replace(2019, "u")

(D) OTHER INFORMATION: /note= "u in ca "master" strain and in
wt2(3)"
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 25..2295

61 (D) OTHER INFORMATION: /product= "polymerase basic 1"
/gene= "PB1"
/note= "polymerase basic 1"
/citation= ([1][2])

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Herlocher, M L
Maassab, H F
Webster, R G

(B) TITLE: Molecular and biological changes in the cold adapted
master strain A/AA/6/60 (H2N2) influenza virus

(C) JOURNAL: Proceedings of the National Academy of Sciences of
the USA

(G) DATE: 1993

(K) RELEVANT RESIDUES IN SEQ ID NO:13: FROM 1 TO 2341

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Cox, N J
Kitame, F
Kendal, A P
Maassab, H F
Naeve, C

(B) TITLE: Identification of sequence changes in the cold-adapted
live attenuated influenza vaccine strain

(C) JOURNAL: Virology

(D) VOLUME: 167

(F) PAGES: 554-567

(G) DATE: 1988

(K) RELEVANT RESIDUES IN SEQ ID NO:13: FROM 1 TO 2341

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AGCGAAAGCA	GGCAAACCAU	UUGA	AUG	GAU	GUC	AAU	CCG	ACC	UUA	CUU	UUC	51				
			Met	Asp	Val	Asn	Pro	Thr	Leu	Leu	Phe					
			1				5									
UUG	AAA	GUU	CCA	GCG	CAA	AAU	GCC	AUA	AGU	ACU	ACA	UUC	CCU	UAU	ACU	99
Leu	Lys	Val	Pro	Ala	Gln	Asn	Ala	Ile	Ser	Thr	Thr	Phe	Pro	Tyr	Thr	
10				15				20				25				

GGA	GAU	CCU	CCA	UAC	AGC	CAU	GGG	ACA	GGA	ACA	GGA	UAC	ACC	AUG	GAC	147
Gly	Asp	Pro	Pro	Tyr	Ser	His	Gly	Thr	Gly	Thr	Gly	Tyr	Thr	Met	Asp	
				30					35					40		
ACA	GUC	AAC	AGA	ACA	CAU	CAA	UAU	UCA	GAA	AAG	GGG	AAG	UGG	ACA	ACA	195
Thr	Val	Asn	Arg	Thr	His	Gln	Tyr	Ser	Glu	Lys	Gly	Lys	Trp	Thr	Thr	
			45					50					55			
AAC	ACG	GAA	ACU	GGA	GCG	CAC	CAA	CUU	AAC	CCA	AUU	GAU	GGA	CCA	CUA	243
Asn	Thr	Glu	Thr	Gly	Ala	His	Gln	Leu	Asn	Pro	Ile	Asp	Gly	Pro	Leu	
		60					65					70				
CCU	GAG	GAC	AAU	GAA	CCA	AGU	GGA	UAU	GCA	CAA	ACA	GAC	UGC	GUC	CUG	291
Pro	Glu	Asp	Asn	Glu	Pro	Ser	Gly	Tyr	Ala	Gln	Thr	Asp	Cys	Val	Leu	
	75					80					85					
GAA	GCA	AUG	GCU	UUC	CUU	GAA	GAA	UCC	CAC	CCA	GGA	AUC	UUU	GAA	AAC	339
Glu	Ala	Met	Ala	Phe	Leu	Glu	Glu	Ser	His	Pro	Gly	Ile	Phe	Glu	Asn	
90					95					100					105	
UCG	UGU	CUU	GAA	ACG	AUG	GAA	GUU	AUU	CAA	CAA	ACA	AGA	GUG	GAC	AAA	387
Ser	Cys	Leu	Glu	Thr	Met	Glu	Val	Ile	Gln	Gln	Thr	Arg	Val	Asp	Lys	
				110					115					120		
CUG	ACC	CAA	GGU	CGU	CAG	ACC	UAU	GAU	UGG	ACA	UUG	AAC	AGA	AAU	CAG	435
Leu	Thr	Gln	Gly	Arg	Gln	Thr	Tyr	Asp	Trp	Thr	Leu	Asn	Arg	Asn	Gln	
			125					130					135			
CCG	GCU	GCA	ACU	GCG	CUA	GCC	AAC	ACU	AUA	GAG	GUC	UUC	AGA	UCG	AAU	483
Pro	Ala	Ala	Thr	Ala	Leu	Ala	Asn	Thr	Ile	Glu	Val	Phe	Arg	Ser	Asn	
		140					145					150				
GGU	CUG	ACA	GCU	AAU	GAA	UCG	GGA	AGG	CUA	AUA	GAU	UUC	CUC	AAG	GAU	531
Gly	Leu	Thr	Ala	Asn	Glu	Ser	Gly	Arg	Leu	Ile	Asp	Phe	Leu	Lys	Asp	
	155					160					165					
GUG	AUA	GAA	UCA	AUG	GAU	AAA	GAG	GAG	AUG	GAA	AUC	ACA	ACA	CAC	UUC	579
Val	Ile	Glu	Ser	Met	Asp	Lys	Glu	Glu	Met	Glu	Ile	Thr	Thr	His	Phe	
170					175					180					185	
CAA	AGA	AAA	AGA	AGA	GUA	AGA	GAC	AAC	AUG	ACC	AAG	AAA	AUG	GUC	ACA	627
Gln	Arg	Lys	Arg	Arg	Val	Arg	Asp	Asn	Met	Thr	Lys	Lys	Met	Val	Thr	
				190					195					200		
CAA	CGA	ACA	AUA	GGA	AAG	AAG	AAG	CAA	AGA	UUG	AAC	AAG	AGA	AGC	UAU	675
Gln	Arg	Thr	Ile	Gly	Lys	Lys	Lys	Gln	Arg	Leu	Asn	Lys	Arg	Ser	Tyr	
			205					210					215			
CUA	AUA	AGA	GCA	CUG	ACA	UUG	AAC	ACA	AUG	ACU	AAA	GAU	GCA	GAG	AGA	723
Leu	Ile	Arg	Ala	Leu	Thr	Leu	Asn	Thr	Met	Thr	Lys	Asp	Ala	Glu	Arg	
		220					225					230				
GGU	AAA	UUA	AAG	AGA	AGA	GCA	AUU	GCA	ACA	CCC	GGU	AUG	CAG	AUC	AGA	771
Gly	Lys	Leu	Lys	Arg	Arg	Ala	Ile	Ala	Thr	Pro	Gly	Met	Gln	Ile	Arg	
	235					240					245					

GGG Gly 250	UUC Phe	GUG Val	UAC Tyr	UUU Phe 255	GUC Val 255	GAA Glu	ACA Thr	CUA Leu	GCG Ala 260	AGA Arg	AGU Ser	AUU Ile	UGU Cys	GAG Glu 265	AAG Lys	819
CUU Leu	GAA Glu	CAG Gln	UCU Ser	GGG Gly 270	CUU Leu	CCG Pro	GUU Val	GGA Gly	GGU Gly 275	AAU Asn	GAA Glu	AAG Lys	AAG Lys	GCU Ala 280	AAA Lys	867
CUG Leu	GCA Ala	AAU Asn	GUU Val 285	GUG Val	CGA Arg	AAA Lys	AUG Met	AUG Met 290	ACU Thr	AAU Asn	UCA Ser	CAA Gln	GAC Asp 295	ACA Thr	GAG Glu	915
CUC Leu	UCU Ser	UUC Phe 300	ACA Thr	AUU Ile	ACU Thr	GGA Gly	GAC Asp 305	AAU Asn	ACC Thr	AAA Lys	UGG Trp	AAU Asn 310	GAG Glu	AAU Asn	CAA Gln	963
AAU Asn 315	CCU Pro	CGG Arg	AUG Met	UUC Phe	CUG Leu	GCG Ala 320	AUG Met	AUA Ile	ACA Thr	UAC Tyr	AUC Ile 325	ACA Thr	AGA Arg	AAU Asn	CAA Gln	1011
CCU Pro 330	GAA Glu	UGG Trp	UUU Phe	AGA Arg	AAC Asn 335	GUC Val	CUG Leu	AGC Ser	AUC Ile	GCA Ala 340	CCU Pro	AUA Ile	AUG Met	UUC Phe	UCA Ser 345	1059
AAU Asn	AAA Lys	AUG Met	GCA Ala	AGA Arg 350	CUA Leu	GGG Gly	AAA Lys	GGA Gly	UAC Tyr 355	AUG Met	UUC Phe	AAA Lys	AGC Ser	AAG Lys 360	AGC Ser	1107
AUG Met	AAG Lys	CUC Leu	CGA Arg 365	ACA Thr	CAA Gln	AUA Ile	CCA Pro	GCA Ala 370	GAA Glu	AUG Met	CUA Leu	GCA Ala	AGU Ser 375	AUU Ile	GAC Asp	1155
CUG Leu	AAA Lys	UAC Tyr 380	UUU Phe	AAU Asn	GAA Glu	UCA Ser	ACA Thr 385	AGA Arg	AAG Lys	AAA Lys	AUC Ile 390	GAG Glu	GAA Glu	AUA Ile	AGG Arg	1203
CCU Pro 395	CUC Leu	CUA Leu	AUA Ile	GAU Asp	GGC Gly	ACA Thr 400	GUC Val	UCA Ser	UUG Leu	AGU Ser	CCU Pro 405	GGA Gly	AUG Met	AUG Met	AUG Met	1251
GGC Gly 410	AUG Met	UUC Phe	AAC Asn	AUG Met	CUA Leu 415	AGU Ser	ACA Thr	GUC Val	UUA Leu	GGA Gly 420	GUC Val	UCA Ser	AUC Ile	CUG Leu	AAU Asn 425	1299
CUU Leu	GGA Gly	CAA Gln	AAG Lys	AAG Lys 430	UAC Tyr	ACC Thr	AAA Lys	ACA Thr	ACA Thr 435	UAC Tyr	UGG Trp	UGG Trp	GAC Asp	GGA Gly 440	CUC Leu	1347
CAA Gln	UCC Ser	UCU Ser	GAU Asp 445	GAC Asp	UUC Phe	GCC Ala	CUC Leu	AUA Ile 450	GUG Val	AAU Asn	GCA Ala	CCA Pro	AAU Asn 455	CAU His	GAU Asp	1395
GGA Gly	AUA Ile	CAA Gln 460	GCA Ala	GGG Gly	GUG Val	GAU Asp	AGA Arg 465	UUC Phe	UAC Tyr	AGA Arg	ACC Thr	UGC Cys 470	AAG Lys	CUA Leu	GUC Val	1443

GGA Gly	AUC Ile	AAU Asn	AUG Met	AGC Ser	AAA Lys	AAG Lys	AAG Lys	UCC Ser	UAC Tyr	AUA Ile	AAU Asn	AGG Arg	ACA Thr	GGG Gly	ACA Thr	1491
475						480					485					
UUU Phe	GAA Glu	UUC Phe	ACA Thr	AGC Ser	UUU Phe	UUC Phe	UAU Tyr	CGC Arg	UAU Tyr	GGA Gly	UUU Phe	GUA Val	GCC Ala	AAU Asn	UUU Phe	1539
490					495					500					505	
AGC Ser	AUG Met	GAG Glu	CUG Leu	CCC Pro	AGC Ser	UUU Phe	GGA Gly	GUG Val	UCU Ser	GGA Gly	AUU Ile	AAU Asn	GAA Glu	UCG Ser	GCU Ala	1587
				510					515					520		
GAU Asp	AUG Met	AGC Ser	AUU Ile	GGG Gly	GUA Val	ACA Thr	GUG Val	AUA Ile	AAG Lys	AAC Asn	AAC Asn	AUG Met	AUA Ile	AAC Asn	AAU Asn	1635
			525					530					535			
GAC Asp	CUU Leu	GGG Gly	CCA Pro	GCA Ala	ACA Thr	GCC Ala	CAA Gln	CUG Leu	GCU Ala	CUU Leu	CAA Gln	CUA Leu	UUC Phe	AUC Ile	AAA Lys	1683
		540					545					550				
GAC Asp	UAC Tyr	AGA Arg	UAU Tyr	ACG Thr	UAC Tyr	CGG Arg	UGC Cys	CAC His	AGA Arg	GGA Gly	GAC Asp	ACA Thr	CAA Gln	AUU Ile	CAG Gln	1731
	555					560					565					
ACA Thr	AGG Arg	AGA Arg	UCA Ser	UUC Phe	GAG Glu	CUA Leu	AAG Lys	AAG Lys	CUG Leu	UGG Trp	GGG Gly	CAA Gln	ACC Thr	CGC Arg	UCA Ser	1779
570					575					580					585	
AAG Lys	GCA Ala	GGA Gly	CUU Leu	UUG Leu	GUU Val	UCG Ser	GAU Asp	GGA Gly	GGA Gly	CCA Pro	AAC Asn	UUA Leu	UAC Tyr	AAU Asn	AUC Ile	1827
				590					595					600		
CGG Arg	AAU Asn	CUC Leu	CAC His	AUU Ile	CCA Pro	GAA Glu	GUC Val	UGC Cys	UUG Leu	AAG Lys	UGG Trp	GAG Glu	CUA Leu	AUG Met	GAU Asp	1875
			605					610					615			
GAA Glu	GAC Asp	UAU Tyr	CAG Gln	GGG Gly	AGG Arg	CUU Leu	UGU Cys	AAU Asn	CCC Pro	CUG Leu	AAU Asn	CCA Pro	UUU Phe	GUC Val	AGU Ser	1923
		620					625					630				
CAU His	AAG Lys	GAG Glu	AUU Ile	GAG Glu	UCU Ser	GUA Val	AAC Asn	AAU Asn	GCU Ala	GUG Val	GUA Val	AUG Met	CCA Pro	GCU Ala	CAC His	1971
	635					640					645					
GGU Gly	CCA Pro	GCC Ala	AAG Lys	AGC Ser	AUG Met	GAA Glu	UAU Tyr	GAU Asp	GCU Ala	GUU Val	ACU Thr	ACU Thr	ACA Thr	CAC His	UCU Ser	2019
650					655					660					665	
UGG Trp	AUC Ile	CCU Pro	AAG Lys	AGG Arg	AAC Asn	CGC Arg	UCC Ser	AUU Ile	CUC Leu	AAC Asn	ACA Thr	AGC Ser	CAA Gln	AGG Arg	GGA Gly	2067
				670					675					680		
AUU Ile	CUU Leu	GAA Glu	GAU Asp	GAA Glu	CAG Gln	AUG Met	UAU Tyr	CAG Gln	AAG Lys	UGU Cys	UGC Cys	AAU Asn	CUA Leu	UUC Phe	GAG Glu	2115
			685					690					695			

AAA UUC UUC CCU AGC AGU UCG UAC AGG AGA CCA GUU GGA AUU UCC AGC 2163
 Lys Phe Phe Pro Ser Ser Ser Tyr Arg Arg Pro Val Gly Ile Ser Ser
 700 705 710

AUG GUG GAG GCC AUG GUG UCU AGG GCC CGG AUU GAU GCA CGG AUU GAC 2211
 Met Val Glu Ala Met Val Ser Arg Ala Arg Ile Asp Ala Arg Ile Asp
 715 720 725

UUC GAG UCU GGA CGG AUU AAG AAA GAG GAG UUC GCU GAG AUC AUG AAG 2259
 Phe Glu Ser Gly Arg Ile Lys Lys Glu Glu Phe Ala Glu Ile Met Lys
 730 735 740 745

AUC UGU UCC ACC AUU GAA GAG CUC AGA CGG CAA AAA UAGUGAAUUU 2305
 Ile Cys Ser Thr Ile Glu Glu Leu Arg Arg Gln Lys
 750 755

AGCUUGUCCU UCAUGAAAAA AUGCCUUGUU UCUACU 2341

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 757 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Asp Val Asn Pro Thr Leu Leu Phe Leu Lys Val Pro Ala Gln Asn
 1 5 10 15

Ala Ile Ser Thr Thr Phe Pro Tyr Thr Gly Asp Pro Pro Tyr Ser His
 20 25 30

Gly Thr Gly Thr Gly Tyr Thr Met Asp Thr Val Asn Arg Thr His Gln
 35 40 45

Tyr Ser Glu Lys Gly Lys Trp Thr Thr Asn Thr Glu Thr Gly Ala His
 50 55 60

Gln Leu Asn Pro Ile Asp Gly Pro Leu Pro Glu Asp Asn Glu Pro Ser
 65 70 75 80

Gly Tyr Ala Gln Thr Asp Cys Val Leu Glu Ala Met Ala Phe Leu Glu
 85 90 95

Glu Ser His Pro Gly Ile Phe Glu Asn Ser Cys Leu Glu Thr Met Glu

61

100						105						110					
Val	Ile	Gln	Gln	Thr	Arg	Val	Asp	Lys	Leu	Thr	Gln	Gly	Arg	Gln	Thr		
		115					120					125					
Tyr	Asp	Trp	Thr	Leu	Asn	Arg	Asn	Gln	Pro	Ala	Ala	Thr	Ala	Leu	Ala		
	130					135					140						
Asn	Thr	Ile	Glu	Val	Phe	Arg	Ser	Asn	Gly	Leu	Thr	Ala	Asn	Glu	Ser		
145					150					155					160		
Gly	Arg	Leu	Ile	Asp	Phe	Leu	Lys	Asp	Val	Ile	Glu	Ser	Met	Asp	Lys		
				165					170					175			
Glu	Glu	Met	Glu	Ile	Thr	Thr	His	Phe	Gln	Arg	Lys	Arg	Arg	Val	Arg		
			180					185					190				
Asp	Asn	Met	Thr	Lys	Lys	Met	Val	Thr	Gln	Arg	Thr	Ile	Gly	Lys	Lys		
		195				200						205					
Lys	Gln	Arg	Leu	Asn	Lys	Arg	Ser	Tyr	Leu	Ile	Arg	Ala	Leu	Thr	Leu		
	210					215					220						
Asn	Thr	Met	Thr	Lys	Asp	Ala	Glu	Arg	Gly	Lys	Leu	Lys	Arg	Arg	Ala		
225					230					235					240		
Ile	Ala	Thr	Pro	Gly	Met	Gln	Ile	Arg	Gly	Phe	Val	Tyr	Phe	Val	Glu		
				245					250					255			
Thr	Leu	Ala	Arg	Ser	Ile	Cys	Glu	Lys	Leu	Glu	Gln	Ser	Gly	Leu	Pro		
			260					265					270				
Val	Gly	Gly	Asn	Glu	Lys	Lys	Ala	Lys	Leu	Ala	Asn	Val	Val	Arg	Lys		
		275				280						285					
Met	Met	Thr	Asn	Ser	Gln	Asp	Thr	Glu	Leu	Ser	Phe	Thr	Ile	Thr	Gly		
	290					295					300						
Asp	Asn	Thr	Lys	Trp	Asn	Glu	Asn	Gln	Asn	Pro	Arg	Met	Phe	Leu	Ala		
305					310					315					320		
Met	Ile	Thr	Tyr	Ile	Thr	Arg	Asn	Gln	Pro	Glu	Trp	Phe	Arg	Asn	Val		
				325					330					335			
Leu	Ser	Ile	Ala	Pro	Ile	Met	Phe	Ser	Asn	Lys	Met	Ala	Arg	Leu	Gly		
			340					345					350				
Lys	Gly	Tyr	Met	Phe	Lys	Ser	Lys	Ser	Met	Lys	Leu	Arg	Thr	Gln	Ile		
		355				360						365					
Pro	Ala	Glu	Met	Leu	Ala	Ser	Ile	Asp	Leu	Lys	Tyr	Phe	Asn	Glu	Ser		
	370					375					380						
Thr	Arg	Lys	Lys	Ile	Glu	Glu	Ile	Arg	Pro	Leu	Leu	Ile	Asp	Gly	Thr		
385					390					395					400		

Val Ser Leu Ser Pro Gly Met Met Met Gly Met Phe Asn Met Leu Ser
 405 410 415
 Thr Val Leu Gly Val Ser Ile Leu Asn Leu Gly Gln Lys Lys Tyr Thr
 420 425 430
 Lys Thr Thr Tyr Trp Trp Asp Gly Leu Gln Ser Ser Asp Asp Phe Ala
 435 440 445
 Leu Ile Val Asn Ala Pro Asn His Asp Gly Ile Gln Ala Gly Val Asp
 450 455 460
 Arg Phe Tyr Arg Thr Cys Lys Leu Val Gly Ile Asn Met Ser Lys Lys
 465 470 475 480
 Lys Ser Tyr Ile Asn Arg Thr Gly Thr Phe Glu Phe Thr Ser Phe Phe
 485 490 495
 Tyr Arg Tyr Gly Phe Val Ala Asn Phe Ser Met Glu Leu Pro Ser Phe
 500 505 510
 Gly Val Ser Gly Ile Asn Glu Ser Ala Asp Met Ser Ile Gly Val Thr
 515 520 525
 Val Ile Lys Asn Asn Met Ile Asn Asn Asp Leu Gly Pro Ala Thr Ala
 530 535 540
 Gln Leu Ala Leu Gln Leu Phe Ile Lys Asp Tyr Arg Tyr Thr Tyr Arg
 545 550 555 560
 Cys His Arg Gly Asp Thr Gln Ile Gln Thr Arg Arg Ser Phe Glu Leu
 565 570 575
 Lys Lys Leu Trp Gly Gln Thr Arg Ser Lys Ala Gly Leu Leu Val Ser
 580 585 590
 Asp Gly Gly Pro Asn Leu Tyr Asn Ile Arg Asn Leu His Ile Pro Glu
 595 600 605
 Val Cys Leu Lys Trp Glu Leu Met Asp Glu Asp Tyr Gln Gly Arg Leu
 610 615 620
 Cys Asn Pro Leu Asn Pro Phe Val Ser His Lys Glu Ile Glu Ser Val
 625 630 635 640
 Asn Asn Ala Val Val Met Pro Ala His Gly Pro Ala Lys Ser Met Glu
 645 650 655
 Tyr Asp Ala Val Thr Thr Thr His Ser Trp Ile Pro Lys Arg Asn Arg
 660 665 670
 Ser Ile Leu Asn Thr Ser Gln Arg Gly Ile Leu Glu Asp Glu Gln Met
 675 680 685
 Tyr Gln Lys Cys Cys Asn Leu Phe Glu Lys Phe Phe Pro Ser Ser Ser

690 695 700

01 Tyr Arg Arg Pro Val Gly Ile Ser Ser Met Val Glu Ala Met Val Ser
705 710 715 720

Arg Ala Arg Ile Asp Ala Arg Ile Asp Phe Glu Ser Gly Arg Ile Lys
725 730 735

Lys Glu Glu Phe Ala Glu Ile Met Lys Ile Cys Ser Thr Ile Glu Glu
740 745 750

Leu Arg Arg Gln Lys
755

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2341 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Influenza virus
- (B) STRAIN: cold-adapted "Master Strain" A/Ann Arbor/6/60 7PI (H2N2)

(vii) IMMEDIATE SOURCE:

- (B) CLONE: PB2

(ix) FEATURE:

- (A) NAME/KEY: mutation
- (B) LOCATION: replace(141, "g")
- (D) OTHER INFORMATION: /note= "g in ca "master" strain; a in wt2(3); g in 1988 reported ca vaccine strain"
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: conflict

(B) LOCATION: replace(426, "c")

(D) OTHER INFORMATION: /note= "c in ca "master" strain and in
wt2(3)"
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: conflict

(B) LOCATION: replace(714, "u")

(D) OTHER INFORMATION: /note= "u in ca "master" strain and in
wt2(3); c in 1988 reported ca vaccine
strain"
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: conflict

(B) LOCATION: replace(821, "g")

(D) OTHER INFORMATION: /note= "g in ca "master" strain and in
wt2(3)"
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: conflict

(B) LOCATION: replace(963, "g")

(D) OTHER INFORMATION: /note= "g in ca "master" strain and in
wt2(3); a in 1988 reported ca vaccine
strain"
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: conflict

(B) LOCATION: replace(1182, "u")

(D) OTHER INFORMATION: /note= "u in ca "master" strain and in
wt2(3)"
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: conflict

(B) LOCATION: replace(1212, "u")

(D) OTHER INFORMATION: /note= "u in ca "master" strain and in
wt2(3)"
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: conflict

(B) LOCATION: replace(1353, "g")

(D) OTHER INFORMATION: /note= "g in ca "master" strain and in
wt2(3)"
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: conflict

(B) LOCATION: replace(1923, "g")

(D) OTHER INFORMATION: /note= "g in ca "master" strain and in
wt2(3)"
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: mutation

(B) LOCATION: replace(1933, "c")

(D) OTHER INFORMATION: /note= "c in ca "master" strain; u in
wt2(3); u in 1988 reported ca vaccine
strain"
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 28..2304

(D) OTHER INFORMATION: /product= "polymerase basic 2"
/gene= "PB2"
/note= "polymerase basic 2"
/citation= ([1][2])

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Herlocher, M L
Maassab, H F
Webster, R G

(B) TITLE: Molecular and biological changes in the cold adapted
master strain A/AA/6/60 (H2N2) influenza virus

(C) JOURNAL: Proceedings of the National Academy of Sciences of
the USA

(G) DATE: 1993

(K) RELEVANT RESIDUES IN SEQ ID NO:15: FROM 1 TO 2341

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Cox, N J
Kitame, F
Kendal, A P
Maassab, H F
Naeve, C

(B) TITLE: Identification of sequence changes in the cold-adapted
live attenuated influenza vaccine strain, A/Ann
Arbor/6/60(H2N2)

(C) JOURNAL: Virology

(D) VOLUME: 167

(F) PAGES: 554-567

(G) DATE: 1988

(K) RELEVANT RESIDUES IN SEQ ID NO:15: FROM 1 TO 2341

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

AGCGAAAGCA	GGUCAUUUAU	AUUCAAU	AUG	GAA	AGA	AUA	AAA	GAA	CUA	CGG	51					
			Met	Glu	Arg	Ile	Lys	Glu	Leu	Arg						
			1				5									
AAU	CUG	AUG	UCG	CAG	UCU	CGC	ACU	CGC	GAG	AUA	CUA	ACA	AAA	ACC	ACA	99
Asn	Leu	Met	Ser	Gln	Ser	Arg	Thr	Arg	Glu	Ile	Leu	Thr	Lys	Thr	Thr	
	10					15					20					
GUG	GAC	CAU	AUG	GCC	AUA	AUU	AAG	AAG	UAC	ACA	UCA	GGG	AGG	CAG	GAA	147
Val	Asp	His	Met	Ala	Ile	Ile	Lys	Lys	Tyr	Thr	Ser	Gly	Arg	Gln	Glu	
	25				30				35					40		
AAG	AAC	CCG	UCA	CUU	AGG	AUG	AAA	UGG	AUG	AUG	GCA	AUG	AAA	UAU	CCG	195

Lys	Asn	Pro	Ser	Leu	Arg	Met	Lys	Trp	Met	Met	Ala	Met	Lys	Tyr	Pro	
				45					50					55		
AUU	ACA	GCC	GAC	AAG	AGG	AUA	ACA	GAA	AUG	AUU	CCU	GAG	AGA	AAU	GAG	243
Ile	Thr	Ala	Asp	Lys	Arg	Ile	Thr	Glu	Met	Ile	Pro	Glu	Arg	Asn	Glu	
			60					65					70			
CAA	GGG	CAA	ACU	CUA	UGG	AGU	AAA	AUG	AGU	GAU	GCC	GGA	UCG	GAU	CGU	291
Gln	Gly	Gln	Thr	Leu	Trp	Ser	Lys	Met	Ser	Asp	Ala	Gly	Ser	Asp	Arg	
		75					80					85				
GUG	AUG	GUA	UCA	CCU	CUG	GCU	GUG	ACA	UGG	UGG	AAU	AGA	AAU	GGA	CCA	339
Val	Met	Val	Ser	Pro	Leu	Ala	Val	Thr	Trp	Trp	Asn	Arg	Asn	Gly	Pro	
	90					95					100					
AUG	ACA	AGU	ACG	GUU	CAU	UAU	CCA	AAA	AUC	UAC	AAA	ACU	UAU	UUU	GAG	387
Met	Thr	Ser	Thr	Val	His	Tyr	Pro	Lys	Ile	Tyr	Lys	Thr	Tyr	Phe	Glu	
105					110					115					120	
AAA	GUC	GAA	AGG	UUA	AAA	CAU	GGA	ACC	UUU	GGC	CCU	GUC	CAU	UUU	AGA	435
Lys	Val	Glu	Arg	Leu	Lys	His	Gly	Thr	Phe	Gly	Pro	Val	His	Phe	Arg	
				125					130					135		
AAC	CAA	GUC	AAA	AUA	CGC	CGA	AGA	GUU	GAC	AUA	AAU	CCU	GGU	CAU	GCA	483
Asn	Gln	Val	Lys	Ile	Arg	Arg	Arg	Val	Asp	Ile	Asn	Pro	Gly	His	Ala	
			140					145					150			
GAC	CUC	AGU	GCC	AAG	GAG	GCA	CAG	GAU	GUA	AUC	AUG	GAA	GUU	GUU	UUC	531
Asp	Leu	Ser	Ala	Lys	Glu	Ala	Gln	Asp	Val	Ile	Met	Glu	Val	Val	Phe	
		155					160					165				
CCU	AAC	GAA	GUG	GGG	GCC	AGG	AUA	CUA	ACG	UCG	GAA	UCG	CAA	UUA	ACA	579
Pro	Asn	Glu	Val	Gly	Ala	Arg	Ile	Leu	Thr	Ser	Glu	Ser	Gln	Leu	Thr	
	170					175					180					
AUA	ACC	AAA	GAG	AAA	AAA	GAA	GAA	CUC	CAG	GAU	UGC	AAA	AUU	UCA	CCU	627
Ile	Thr	Lys	Glu	Lys	Lys	Glu	Glu	Leu	Gln	Asp	Cys	Lys	Ile	Ser	Pro	
185					190					195					200	
UUG	AUG	GUU	GCG	UAC	AUG	UUA	GAG	AGA	GAA	CUU	GUC	CGA	AAA	ACG	AGA	675
Leu	Met	Val	Ala	Tyr	Met	Leu	Glu	Arg	Glu	Leu	Val	Arg	Lys	Thr	Arg	
				205					210					215		
UUU	CUC	CCA	GUU	GCU	GGU	GGA	ACA	AGC	AGU	GUG	UAC	AUU	GAA	GUG	UUG	723
Phe	Leu	Pro	Val	Ala	Gly	Gly	Thr	Ser	Ser	Val	Tyr	Ile	Glu	Val	Leu	
			220					225					230			
CAC	UUG	ACU	CAA	GGA	ACA	UGC	UGG	GAA	CAG	AUG	UAC	ACU	CCA	GGU	GGA	771
His	Leu	Thr	Gln	Gly	Thr	Cys	Trp	Glu	Gln	Met	Tyr	Thr	Pro	Gly	Gly	
		235					240					245				
GAA	GUG	AGG	AAU	GAU	GAU	GUU	GAU	CAA	AGU	CUA	AUU	AUU	GCA	GCC	AGG	819
Glu	Val	Arg	Asn	Asp	Asp	Val	Asp	Gln	Ser	Leu	Ile	Ile	Ala	Ala	Arg	
	250					255					260					

AGC Ser 265	AUA Ile	GUG Val	AGA Arg	AGA Arg	GCA Ala 270	GCA Ala	GUA Val	UCA Ser	GCA Ala	GAU Asp 275	CCA Pro	CUA Leu	GCA Ala	UCU Ser	UUA Leu 280	867
UUG Leu	GAG Glu	AUG Met	UGC Cys	CAC His 285	AGC Ser	ACA Thr	CAG Gln	AUU Ile	GGC Gly 290	GGG Gly	ACA Thr	AGG Arg	AUG Met	GUG Val 295	GAC Asp	915
AUU Ile	CUU Leu	AGG Arg	CAG Gln 300	AAC Asn	CCA Pro	ACA Thr	GAA Glu	GAG Glu 305	CAA Gln	GCU Ala	GUG Val	GAA Glu	AUA Ile 310	UGC Cys	AAG Lys	963
GCU Ala	GCA Ala	AUG Met 315	GGA Gly	CUG Leu	AGG Arg	AUC Ile	AGC Ser 320	UCA Ser	UCC Ser	UUC Phe	AGU Ser	UUU Phe 325	GGC Gly	GGG Gly	UUC Phe	1011
ACA Thr 330	UUU Phe	AAG Lys	AGA Arg	ACA Thr	AGC Ser	GGA Gly 335	UCA Ser	UCA Ser	GUC Val	AAG Lys	AGA Arg 340	GAG Glu	GAA Glu	GAA Glu	GUG Val	1059
CUU Leu 345	ACG Thr	GGC Gly	AAU Asn	CUU Leu	CAA Gln 350	ACA Thr	UUG Leu	AAA Lys	AUA Ile	AGG Arg 355	GUG Val	CAU His	GAG Glu	GGA Gly	UAC Tyr 360	1107
GAG Glu	GAG Glu	UUC Phe	ACA Thr	AUG Met 365	GUU Val	GGG Gly	AAA Lys	AGG Arg	GCA Ala 370	ACA Thr	GCU Ala	AUA Ile	CUC Leu	AGA Arg 375	AAA Lys	1155
GCA Ala	ACC Thr	AGG Arg	AGA Arg 380	UUG Leu	AUU Ile	CAG Gln	CUG Leu	AUU Ile 385	GUG Val	AGU Ser	GGA Gly	AGA Arg 390	GAC Asp	GAA Glu	CAG Gln	1203
UCG Ser	AUA Ile 395	GCU Ala	GAA Glu	GCA Ala	AUA Ile	AUU Ile	GUG Val 400	GCC Ala	AUG Met	GUA Val	UUU Phe 405	UCA Ser	CAA Gln	GAA Glu	GAU Asp	1251
UGU Cys 410	AUG Met	AUA Ile	AAA Lys	GCA Ala	GUU Val	AGA Arg 415	GGU Gly	GAU Asp	CUG Leu	AAU Asn	UUC Phe 420	GUU Val	AAU Asn	AGG Arg	GCA Ala	1299
AAU Asn 425	CAG Gln	CGA Arg	UUG Leu	AAU Asn	CCC Pro 430	AUG Met	CAU His	CAA Gln	CUU Leu	UUA Leu 435	AGA Arg	CAU His	UUU Phe	CAG Gln	AAG Lys 440	1347
GAU Asp	GCG Ala	AAA Lys	GUG Val	CUU Leu 445	UUU Phe	CAA Gln	AAU Asn	UGG Trp 450	GGA Gly	AUU Ile	GAA Glu	CAU His	AUC Ile	GAC Asp 455	AAU Asn	1395
GUG Val	AUG Met	GGA Gly	AUG Met 460	AUU Ile	GGG Gly	GUA Val	UUA Leu	CCA Pro 465	GAC Asp	AUG Met	ACU Thr	CCA Pro	AGC Ser 470	ACA Thr	GAG Glu	1443
AUG Met	UCA Ser	AUG Met 475	AGA Arg	GGG Gly	GUA Val	AGA Arg	GUC Val 480	AGC Ser	AAA Lys	AUG Met	GGC Gly	GUA Val 485	GAU Asp	GAA Glu	UAC Tyr	1491

UCC Ser 490	AGC Ser	GCG Ala	GAG Glu	AGA Arg	GUA Val	GUG Val 495	GUG Val	AGC Ser	AUU Ile	GAC Asp	CGG Arg 500	UUU Phe	UUG Leu	AGA Arg	GUU Val	1539
CGA Arg 505	GAC Asp	CAA Gln	CGA Arg	GGA Gly	AAU Asn 510	GUA Val	CUA Leu	CUA Leu	UCU Ser	CCU Pro 515	GAG Glu	GAG Glu	GUC Val	AGU Ser	GAA Glu 520	1587
ACA Thr	CAG Gln	GGA Gly	ACA Thr	GAG Glu 525	AAA Lys	CUG Leu	ACA Thr	AUA Ile	ACU Thr 530	UAC Tyr	UCA Ser	UCG Ser	UCA Ser	AUG Met 535	AUG Met	1635
UGG Trp	GAG Glu	AUU Ile	AAU Asn 540	GGC Gly	CCU Pro	GAG Glu	UCA Ser	GUG Val 545	UUG Leu	GUC Val	AAU Asn	ACC Thr	UAU Tyr 550	CAG Gln	UGG Trp	1683
AUC Ile	AUC Ile	AGA Arg 555	AAC Asn	UGG Trp	GAA Glu	ACU Thr	GUU Val 560	AAA Lys	AUU Ile	CAG Gln	UGG Trp	UCU Ser	CAG Gln	AAU Asn	CCU Pro	1731
ACA Thr 570	AUG Met	CUA Leu	UAC Tyr	AAU Asn	AAA Lys	AUG Met 575	GAA Glu	UUU Phe	GAG Glu	CCA Pro	UUU Phe 580	CAG Gln	UCU Ser	UUA Leu	GUU Val	1779
CCU Pro 585	AAG Lys	GCC Ala	AUU Ile	AGA Arg	GGC Gly 590	CAA Gln	UAC Tyr	AGU Ser	GGG Gly	UUU Phe 595	GUU Val	AGG Arg	ACU Thr	CUA Leu	UUC Phe 600	1827
CAA Gln	CAA Gln	AUG Met	AGG Arg	GAU Asp 605	GUA Val	CUU Leu	GGG Gly	ACA Thr	UUU Phe 610	GAU Asp	ACC Thr	ACC Thr	CAG Gln	AUA Ile 615	AUA Ile	1875
AAA Lys	CUU Leu	CUU Leu	CCC Pro 620	UUU Phe	GCA Ala	GCC Ala	GCC Ala	CCA Pro 625	CCA Pro	AAG Lys	CAA Gln	AGU Ser	AGA Arg	AUG Met	CAG Gln	1923
UUC Phe	UCU Ser	UCA Ser 635	CUG Leu	ACU Thr	GUG Val	AAU Asn	GUG Val 640	AGG Arg	GGA Gly	UCA Ser	GGA Gly	AUG Met	AGA Arg	AUA Ile	CUU Leu	1971
GUA Val 650	AGG Arg	GGC Gly	AAU Asn	UCU Ser	CCU Pro	AUA Ile 655	UUC Phe	AAC Asn	UAC Tyr	AAC Asn	AAG Lys 660	ACC Thr	ACU Thr	AAG Lys	AGA Arg	2019
CUA Leu 665	ACA Thr	AUU Ile	CUC Leu	GGA Gly	AAG Lys 670	GAU Asp	GCU Ala	GGC Gly	ACU Thr	UUA Leu 675	ACU Thr	GAA Glu	GAC Asp	CCA Pro	GAU Asp 680	2067
GAA Glu	GGC Gly	ACA Thr	UCU Ser	GGA Gly 685	GUG Val	GAG Glu	UCC Ser	GCU Ala	GUU Val 690	CUG Leu	AGA Arg	GGA Gly	UUC Phe	CUC Leu 695	AUU Ile	2115
CUG Leu	GGC Gly	AAA Lys	GAA Glu 700	GAU Asp	AGG Arg	AGA Arg	UAU Tyr	GGA Gly 705	CCA Pro	GCA Ala	UUA Leu	AGC Ser	AUC Ile 710	AAU Asn	GAA Glu	2163

CUG AGU AAC CUU GCG AAA GGA GAA AAG GCU AAU GUA CUA AUU GGG CAA 2211
 Leu Ser Asn Leu Ala Lys Gly Glu Lys Ala Asn Val Leu Ile Gly Gln
 715 720 725
 GGA GAC GUG GUG UUG GUA AUG AAA CGA AAA CGG AAC UCU AGC AUA CUU 2259
 Gly Asp Val Val Leu Val Met Lys Arg Lys Arg Asn Ser Ser Ile Leu
 730 735 740
 ACU GAC AGC CAG ACA GCG ACC AAA AGG AUU CGG AUG GCC AUC AAU 2304
 Thr Asp Ser Gln Thr Ala Thr Lys Arg Ile Arg Met Ala Ile Asn
 745 750 755
 UAAUGUUGAA UAGUUUAAAA ACGACCUUGU UUCUACU 2341

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 759 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met Glu Arg Ile Lys Glu Leu Arg Asn Leu Met Ser Gln Ser Arg Thr
 1 5 10 15
 Arg Glu Ile Leu Thr Lys Thr Thr Val Asp His Met Ala Ile Ile Lys
 20 25 30
 Lys Tyr Thr Ser Gly Arg Gln Glu Lys Asn Pro Ser Leu Arg Met Lys
 35 40 45
 Trp Met Met Ala Met Lys Tyr Pro Ile Thr Ala Asp Lys Arg Ile Thr
 50 55 60
 Glu Met Ile Pro Glu Arg Asn Glu Gln Gly Gln Thr Leu Trp Ser Lys
 65 70 75 80
 Met Ser Asp Ala Gly Ser Asp Arg Val Met Val Ser Pro Leu Ala Val
 85 90 95
 Thr Trp Trp Asn Arg Asn Gly Pro Met Thr Ser Thr Val His Tyr Pro
 100 105 110
 Lys Ile Tyr Lys Thr Tyr Phe Glu Lys Val Glu Arg Leu Lys His Gly
 115 120 125

Thr Phe Gly Pro Val His Phe Arg Asn Gln Val Lys Ile Arg Arg Arg
 130 135 140
 Val Asp Ile Asn Pro Gly His Ala Asp Leu Ser Ala Lys Glu Ala Gln
 145 150 155 160
 Asp Val Ile Met Glu Val Val Phe Pro Asn Glu Val Gly Ala Arg Ile
 165 170 175
 Leu Thr Ser Glu Ser Gln Leu Thr Ile Thr Lys Glu Lys Lys Glu Glu
 180 185 190
 Leu Gln Asp Cys Lys Ile Ser Pro Leu Met Val Ala Tyr Met Leu Glu
 195 200 205
 Arg Glu Leu Val Arg Lys Thr Arg Phe Leu Pro Val Ala Gly Gly Thr
 210 215 220
 Ser Ser Val Tyr Ile Glu Val Leu His Leu Thr Gln Gly Thr Cys Trp
 225 230 235 240
 Glu Gln Met Tyr Thr Pro Gly Gly Glu Val Arg Asn Asp Asp Val Asp
 245 250 255
 Gln Ser Leu Ile Ile Ala Ala Arg Ser Ile Val Arg Arg Ala Ala Val
 260 265 270
 Ser Ala Asp Pro Leu Ala Ser Leu Leu Glu Met Cys His Ser Thr Gln
 275 280 285
 Ile Gly Gly Thr Arg Met Val Asp Ile Leu Arg Gln Asn Pro Thr Glu
 290 295 300
 Glu Gln Ala Val Glu Ile Cys Lys Ala Ala Met Gly Leu Arg Ile Ser
 305 310 315 320
 Ser Ser Phe Ser Phe Gly Gly Phe Thr Phe Lys Arg Thr Ser Gly Ser
 325 330 335
 Ser Val Lys Arg Glu Glu Glu Val Leu Thr Gly Asn Leu Gln Thr Leu
 340 345 350
 Lys Ile Arg Val His Glu Gly Tyr Glu Glu Phe Thr Met Val Gly Lys
 355 360 365
 Arg Ala Thr Ala Ile Leu Arg Lys Ala Thr Arg Arg Leu Ile Gln Leu
 370 375 380
 Ile Val Ser Gly Arg Asp Glu Gln Ser Ile Ala Glu Ala Ile Ile Val
 385 390 395 400
 Ala Met Val Phe Ser Gln Glu Asp Cys Met Ile Lys Ala Val Arg Gly
 405 410 415
 Asp Leu Asn Phe Val Asn Arg Ala Asn Gln Arg Leu Asn Pro Met His
 420 425 430

Gln Leu Leu Arg His Phe Gln Lys Asp Ala Lys Val Leu Phe Gln Asn
 435 440 445
 Trp Gly Ile Glu His Ile Asp Asn Val Met Gly Met Ile Gly Val Leu
 450 455 460
 Pro Asp Met Thr Pro Ser Thr Glu Met Ser Met Arg Gly Val Arg Val
 465 470 475 480
 Ser Lys Met Gly Val Asp Glu Tyr Ser Ser Ala Glu Arg Val Val Val
 485 490 495
 Ser Ile Asp Arg Phe Leu Arg Val Arg Asp Gln Arg Gly Asn Val Leu
 500 505 510
 Leu Ser Pro Glu Glu Val Ser Glu Thr Gln Gly Thr Glu Lys Leu Thr
 515 520 525
 Ile Thr Tyr Ser Ser Ser Met Met Trp Glu Ile Asn Gly Pro Glu Ser
 530 535 540
 Val Leu Val Asn Thr Tyr Gln Trp Ile Ile Arg Asn Trp Glu Thr Val
 545 550 555 560
 Lys Ile Gln Trp Ser Gln Asn Pro Thr Met Leu Tyr Asn Lys Met Glu
 565 570 575
 Phe Glu Pro Phe Gln Ser Leu Val Pro Lys Ala Ile Arg Gly Gln Tyr
 580 585 590
 Ser Gly Phe Val Arg Thr Leu Phe Gln Gln Met Arg Asp Val Leu Gly
 595 600 605
 Thr Phe Asp Thr Thr Gln Ile Ile Lys Leu Leu Pro Phe Ala Ala Ala
 610 615 620
 Pro Pro Lys Gln Ser Arg Met Gln Phe Ser Ser Leu Thr Val Asn Val
 625 630 635 640
 Arg Gly Ser Gly Met Arg Ile Leu Val Arg Gly Asn Ser Pro Ile Phe
 645 650 655
 Asn Tyr Asn Lys Thr Thr Lys Arg Leu Thr Ile Leu Gly Lys Asp Ala
 660 665 670
 Gly Thr Leu Thr Glu Asp Pro Asp Glu Gly Thr Ser Gly Val Glu Ser
 675 680 685
 Ala Val Leu Arg Gly Phe Leu Ile Leu Gly Lys Glu Asp Arg Arg Tyr
 690 695 700
 Gly Pro Ala Leu Ser Ile Asn Glu Leu Ser Asn Leu Ala Lys Gly Glu
 705 710 715 720
 Lys Ala Asn Val Leu Ile Gly Gln Gly Asp Val Val Leu Val Met Lys

725 730 735
Arg Lys Arg Asn Ser Ser Ile Leu Thr Asp Ser Gln Thr Ala Thr Lys
740 745 750
Arg Ile Arg Met Ala Ile Asn
755

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1773 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Influenza virus
- (B) STRAIN: cold-adapted "Master Strain" A/Ann Arbor/6/60 7PI (H2N2)

(vii) IMMEDIATE SOURCE:

- (B) CLONE: HA

(ix) FEATURE:

- (A) NAME/KEY: mutation
- (B) LOCATION: replace(144, "u")
- (D) OTHER INFORMATION: /gene= "HA"
/note= "u in ca "master" strain; a in
w2(3)"
/citation= ([1])

(ix) FEATURE:

- (A) NAME/KEY: mutation

(B) LOCATION: replace(455, "a")

(D) OTHER INFORMATION: /gene= "HA"
/note= "a in ca "master" strain; g in
wt2(3)"
/citation= ([1])

(ix) FEATURE:

(A) NAME/KEY: mutation

(B) LOCATION: replace(729, "c")

(D) OTHER INFORMATION: /gene= "HA"
/note= "c in ca "master" strain; a in
wt2(3)"
/citation= ([1])

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 44..1729

(D) OTHER INFORMATION: /product= "hemagglutinin"
/gene= "HA"
/note= "hemagglutinin protein"
/citation= ([1])

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Herlocher, M L
Maassab, H F
Webster, R G

(B) TITLE: Molecular and biological changes in the cold adapted
master strain A/AA/6/60 (H2N2) influenza virus

(C) JOURNAL: Proceedings of the National Academy of Sciences of
the USA

(G) DATE: 1993

(K) RELEVANT RESIDUES IN SEQ ID NO:17: FROM 1 TO 1773

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

AGCAAAAGCA GGGGUUUAUAC CAUAGACAAC CAAAAGCAAA ACA AUG GCC AUC AUU
Met Ala Ile Ile

1

UAU	CUC	AUU	CUC	CUG	UUC	ACA	GCA	GUG	AGA	GGG	GAC	AAG	AUA	UGC	AUU	103
Tyr	Leu	Ile	Leu	Leu	Phe	Thr	Ala	Val	Arg	Gly	Asp	Lys	Ile	Cys	Ile	
5					10					15					20	
GGA	UAC	CAU	GCC	AAU	AAU	UCC	ACA	GAG	ACG	GUC	GAC	ACA	AUU	CUA	GAG	151
Gly	Tyr	His	Ala	Asn	Asn	Ser	Thr	Glu	Thr	Val	Asp	Thr	Ile	Leu	Glu	
				25				30						35		
CGG	AAC	GUC	ACU	GUG	ACU	CAU	GCC	AAG	GAC	AUU	CUU	GAG	AAG	ACC	CAU	199
Arg	Asn	Val	Thr	Val	Thr	His	Ala	Lys	Asp	Ile	Leu	Glu	Lys	Thr	His	
			40					45					50			
AAC	GGA	AAG	UUA	UGC	AAA	CUA	AAC	GGA	AUC	CCU	CCA	CUU	GAA	CUA	GGG	247
Asn	Gly	Lys	Leu	Cys	Lys	Leu	Asn	Gly	Ile	Pro	Pro	Leu	Glu	Leu	Gly	
		55					60					65				
GAC	UGU	AGC	AUU	GCC	GGA	UGG	CUC	CUU	GGA	AAU	CCA	GAA	UGU	GAU	AGG	295
Asp	Cys	Ser	Ile	Ala	Gly	Trp	Leu	Leu	Gly	Asn	Pro	Glu	Cys	Asp	Arg	
	70				75					80						
CUU	CUA	AGU	GUG	CCA	GAA	UGG	UCC	UAU	AUA	AUG	GAG	AAA	GAA	AAC	CCG	343
Leu	Leu	Ser	Val	Pro	Glu	Trp	Ser	Tyr	Ile	Met	Glu	Lys	Glu	Asn	Pro	
85				90						95					100	
AGA	AAC	GGU	UUG	UGU	UAU	CCA	GGC	AAC	UUC	AAU	GAU	UAU	GAA	GAA	UUG	391
Arg	Asn	Gly	Leu	Cys	Tyr	Pro	Gly	Asn	Phe	Asn	Asp	Tyr	Glu	Glu	Leu	
				105					110					115		
AAA	CAU	CUC	CUC	AGC	AGC	GUG	AAA	CAU	UUC	GAG	AAA	GUA	AAG	AUU	CUG	439
Lys	His	Leu	Leu	Ser	Ser	Val	Lys	His	Phe	Glu	Lys	Val	Lys	Ile	Leu	
			120					125					130			
CCC	AAA	GAU	AGA	UGG	ACA	CAG	CAU	ACA	ACA	ACU	GGA	GGU	UCA	CAG	GCC	487
Pro	Lys	Asp	Arg	Trp	Thr	Gln	His	Thr	Thr	Thr	Gly	Gly	Ser	Gln	Ala	
		135					140					145				
UGC	GCG	GUG	UCU	GGU	AAU	CCA	UCA	UUC	UUC	AGG	AAC	AUG	GUC	UGG	CUG	535
Cys	Ala	Val	Ser	Gly	Asn	Pro	Ser	Phe	Phe	Arg	Asn	Met	Val	Trp	Leu	
	150					155					160					
ACA	GAG	GAA	GGA	UCA	AAU	UAU	CCG	GUU	GCC	AAA	GGA	UCG	UAC	AAC	AAU	583
Thr	Glu	Glu	Gly	Ser	Asn	Tyr	Pro	Val	Ala	Lys	Gly	Ser	Tyr	Asn	Asn	
165				170						175					180	
ACA	AGC	GGA	GAA	CAA	AUG	CUA	AUA	AUU	UGG	GGG	GUG	CAC	CAU	CCC	AUU	631
Thr	Ser	Gly	Glu	Gln	Met	Leu	Ile	Ile	Trp	Gly	Val	His	His	Pro	Ile	
				185					190					195		
GAU	GAG	ACA	GAA	CAA	AGA	ACA	UUG	UAC	CAG	AAU	GUG	GGA	ACC	UAU	GUU	679
Asp	Glu	Thr	Glu	Gln	Arg	Thr	Leu	Tyr	Gln	Asn	Val	Gly	Thr	Tyr	Val	
			200					205					210			
UCC	GUA	GGC	ACA	UCA	ACA	UUG	AAC	AAA	AGG	UCA	ACC	CCA	GAA	AUA	GCA	727

Ser	Val	Gly	Thr	Ser	Thr	Leu	Asn	Lys	Arg	Ser	Thr	Pro	Glu	Ile	Ala	
		215					220					225				
ACA	AGG	CCU	AAA	GUG	AAU	GGA	CUA	GGA	AGU	AGA	AUG	GAA	UUC	UCU	UGG	775
Thr	Arg	Pro	Lys	Val	Asn	Gly	Leu	Gly	Ser	Arg	Met	Glu	Phe	Ser	Trp	
	230					235					240					
ACC	CUC	UUG	GAU	AUG	UGG	GAC	ACC	AUA	AAU	UUU	GAG	AGU	ACU	GGU	AAU	823
Thr	Leu	Leu	Asp	Met	Trp	Asp	Thr	Ile	Asn	Phe	Glu	Ser	Thr	Gly	Asn	
	245				250					255					260	
CUA	AUU	GCA	CCA	GAG	UAU	GGA	UUC	AAA	AUA	UCG	AAA	AGA	GGU	AGU	UCU	871
Leu	Ile	Ala	Pro	Glu	Tyr	Gly	Phe	Lys	Ile	Ser	Lys	Arg	Gly	Ser	Ser	
				265					270					275		
GGG	AUC	AUG	AAA	ACA	GAA	GGA	ACA	CUU	GAG	AAC	UGU	GAG	ACC	AAA	UGC	919
Gly	Ile	Met	Lys	Thr	Glu	Gly	Thr	Leu	Glu	Asn	Cys	Glu	Thr	Lys	Cys	
			280					285					290			
CAA	ACU	CCU	UUG	GGA	GCA	AUA	AAU	ACA	ACA	UUG	CCU	UUU	CAC	AAU	GUC	967
Gln	Thr	Pro	Leu	Gly	Ala	Ile	Asn	Thr	Thr	Leu	Pro	Phe	His	Asn	Val	
		295					300					305				
CAC	CCA	CUG	ACA	AUA	GGU	GAG	UGC	CCC	AAA	UAU	GUA	AAA	UCG	GAG	AAG	1015
His	Pro	Leu	Thr	Ile	Gly	Glu	Cys	Pro	Lys	Tyr	Val	Lys	Ser	Glu	Lys	
	310					315					320					
UUG	GUC	UUA	GCA	ACA	GGA	CUA	AGG	AAU	GUU	CCC	CAG	AUU	GAA	UCA	AGA	1063
Leu	Val	Leu	Ala	Thr	Gly	Leu	Arg	Asn	Val	Pro	Gln	Ile	Glu	Ser	Arg	
	325				330					335					340	
GGA	UUG	UUU	GGG	GCA	AUA	GCU	GGU	UUU	AUA	GAA	GGA	GGA	UGG	CAA	GGA	1111
Gly	Leu	Phe	Gly	Ala	Ile	Ala	Gly	Phe	Ile	Glu	Gly	Gly	Trp	Gln	Gly	
				345					350					355		
AUG	GUU	GAU	GGU	UGG	UAU	GGA	UAC	CAU	CAC	AGC	AAU	GAC	CAG	GGU	UCA	1159
Met	Val	Asp	Gly	Trp	Tyr	Gly	Tyr	His	His	Ser	Asn	Asp	Gln	Gly	Ser	
			360					365					370			
GGG	UAU	GCA	GCA	GAC	AAA	GAA	UCC	ACU	CAA	AAG	GCA	UUU	GAU	GGA	AUC	1207
Gly	Tyr	Ala	Ala	Asp	Lys	Glu	Ser	Thr	Gln	Lys	Ala	Phe	Asp	Gly	Ile	
		375					380					385				
ACC	AAC	AAG	GUA	AAU	UCU	GUG	AUU	GAA	AAG	AUA	AAC	ACC	CAA	UUU	GAA	1255
Thr	Asn	Lys	Val	Asn	Ser	Val	Ile	Glu	Lys	Ile	Asn	Thr	Gln	Phe	Glu	
	390					395					400					
GCU	GUU	GGG	AAA	GAA	UUC	AGU	AAC	UUA	GAG	AGA	AGA	CUG	GAG	AAC	UUG	1303
Ala	Val	Gly	Lys	Glu	Phe	Ser	Asn	Leu	Glu	Arg	Arg	Leu	Glu	Asn	Leu	
	405				410					415					420	
AAC	AAA	AAG	AUG	GAA	GAC	GGG	UUU	CUA	GAU	GUG	UGG	ACA	UAC	AAU	GCU	1351
Asn	Lys	Lys	Met	Glu	Asp	Gly	Phe	Leu	Asp	Val	Trp	Thr	Tyr	Asn	Ala	
				425					430					435		

GAG	CUU	CUA	GUU	CUG	AUG	GAA	AAU	GAG	AGG	ACA	CUU	GAC	UUU	CAU	GAU	1399
Glu	Leu	Leu	Val	Leu	Met	Glu	Asn	Glu	Arg	Thr	Leu	Asp	Phe	His	Asp	
			440					445					450			
UCU	AAU	GUC	AAG	AAU	CUG	UAU	GAU	AAA	GUC	AGA	AUG	CAG	CUG	AGG	GAC	1447
Ser	Asn	Val	Lys	Asn	Leu	Tyr	Asp	Lys	Val	Arg	Met	Gln	Leu	Arg	Asp	
		455					460					465				
AAC	GUC	AAA	GAA	CUA	GGA	AAU	GGA	UGU	UUU	GAA	UUU	UAU	CAC	AAA	UGU	1495
Asn	Val	Lys	Glu	Leu	Gly	Asn	Gly	Cys	Phe	Glu	Phe	Tyr	His	Lys	Cys	
	470					475					480					
GAU	GAU	GAA	UGC	AUG	AAU	AGU	GUG	AAA	AAC	GGG	ACA	UAU	GAU	UAU	CCC	1543
Asp	Asp	Glu	Cys	Met	Asn	Ser	Val	Lys	Asn	Gly	Thr	Tyr	Asp	Tyr	Pro	
485					490					495					500	
AAG	UAU	GAA	GAA	GAG	UCU	AAA	CUA	AAU	AGA	AAU	GAA	AUU	AAA	GGG	GUA	1591
Lys	Tyr	Glu	Glu	Glu	Ser	Lys	Leu	Asn	Arg	Asn	Glu	Ile	Lys	Gly	Val	
			505						510					515		
AAA	UUG	AGC	AGC	AUG	GGG	GUU	UGU	CGG	AUC	CUU	GCC	AUU	UAU	GCU	ACA	1639
Lys	Leu	Ser	Ser	Met	Gly	Val	Cys	Arg	Ile	Leu	Ala	Ile	Tyr	Ala	Thr	
			520					525					530			
GUA	GCA	GGU	UCU	CUG	UCA	CUG	GCA	AUC	AUG	AUG	GCU	GGG	AUC	UCU	UUC	1687
Val	Ala	Gly	Ser	Leu	Ser	Leu	Ala	Ile	Met	Met	Ala	Gly	Ile	Ser	Phe	
		535					540					545				
UGG	AUG	UGC	UCC	AAC	GGG	UCU	CUG	CAG	UGC	AGG	AUC	UGC	AUA			1729
Trp	Met	Cys	Ser	Asn	Gly	Ser	Leu	Gln	Cys	Arg	Ile	Cys	Ile			
	550					555					560					
UGAUUUAAG UCAUUUUUAU AUUAAAAACA CCCUUGUUUC UACU																1773

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 562 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Met Ala Ile Ile Tyr Leu Ile Leu Leu Phe Thr Ala Val Arg Gly Asp
 1 5 10 15

Lys Ile Cys Ile Gly Tyr His Ala Asn Asn Ser Thr Glu Thr Val Asp
 20 25 30
 Thr Ile Leu Glu Arg Asn Val Thr Val Thr His Ala Lys Asp Ile Leu
 35 40 45
 Glu Lys Thr His Asn Gly Lys Leu Cys Lys Leu Asn Gly Ile Pro Pro
 50 55 60
 Leu Glu Leu Gly Asp Cys Ser Ile Ala Gly Trp Leu Leu Gly Asn Pro
 65 70 75 80
 Glu Cys Asp Arg Leu Leu Ser Val Pro Glu Trp Ser Tyr Ile Met Glu
 85 90 95
 Lys Glu Asn Pro Arg Asn Gly Leu Cys Tyr Pro Gly Asn Phe Asn Asp
 100 105 110
 Tyr Glu Glu Leu Lys His Leu Leu Ser Ser Val Lys His Phe Glu Lys
 115 120 125
 Val Lys Ile Leu Pro Lys Asp Arg Trp Thr Gln His Thr Thr Thr Gly
 130 135 140
 Gly Ser Gln Ala Cys Ala Val Ser Gly Asn Pro Ser Phe Phe Arg Asn
 145 150 155 160
 Met Val Trp Leu Thr Glu Glu Gly Ser Asn Tyr Pro Val Ala Lys Gly
 165 170 175
 Ser Tyr Asn Asn Thr Ser Gly Glu Gln Met Leu Ile Ile Trp Gly Val
 180 185 190
 His His Pro Ile Asp Glu Thr Glu Gln Arg Thr Leu Tyr Gln Asn Val
 195 200 205
 Gly Thr Tyr Val Ser Val Gly Thr Ser Thr Leu Asn Lys Arg Ser Thr
 210 215 220
 Pro Glu Ile Ala Thr Arg Pro Lys Val Asn Gly Leu Gly Ser Arg Met
 225 230 235 240
 Glu Phe Ser Trp Thr Leu Leu Asp Met Trp Asp Thr Ile Asn Phe Glu
 245 250 255
 Ser Thr Gly Asn Leu Ile Ala Pro Glu Tyr Gly Phe Lys Ile Ser Lys
 260 265 270
 Arg Gly Ser Ser Gly Ile Met Lys Thr Glu Gly Thr Leu Glu Asn Cys
 275 280 285
 Glu Thr Lys Cys Gln Thr Pro Leu Gly Ala Ile Asn Thr Thr Leu Pro
 290 295 300
 Phe His Asn Val His Pro Leu Thr Ile Gly Glu Cys Pro Lys Tyr Val

305 310 315 320
 Lys Ser Glu Lys Leu Val Leu Ala Thr Gly Leu Arg Asn Val Pro Gln
 325 330 335
 Ile Glu Ser Arg Gly Leu Phe Gly Ala Ile Ala Gly Phe Ile Glu Gly
 340 345 350
 Gly Trp Gln Gly Met Val Asp Gly Trp Tyr Gly Tyr His His Ser Asn
 355 360 365
 Asp Gln Gly Ser Gly Tyr Ala Ala Asp Lys Glu Ser Thr Gln Lys Ala
 370 375 380
 Phe Asp Gly Ile Thr Asn Lys Val Asn Ser Val Ile Glu Lys Ile Asn
 385 390 395 400
 Thr Gln Phe Glu Ala Val Gly Lys Glu Phe Ser Asn Leu Glu Arg Arg
 405 410 415
 Leu Glu Asn Leu Asn Lys Lys Met Glu Asp Gly Phe Leu Asp Val Trp
 420 425 430
 Thr Tyr Asn Ala Glu Leu Leu Val Leu Met Glu Asn Glu Arg Thr Leu
 435 440 445
 Asp Phe His Asp Ser Asn Val Lys Asn Leu Tyr Asp Lys Val Arg Met
 450 455 460
 Gln Leu Arg Asp Asn Val Lys Glu Leu Gly Asn Gly Cys Phe Glu Phe
 465 470 475 480
 Tyr His Lys Cys Asp Asp Glu Cys Met Asn Ser Val Lys Asn Gly Thr
 485 490 495
 Tyr Asp Tyr Pro Lys Tyr Glu Glu Glu Ser Lys Leu Asn Arg Asn Glu
 500 505 510
 Ile Lys Gly Val Lys Leu Ser Ser Met Gly Val Cys Arg Ile Leu Ala
 515 520 525
 Ile Tyr Ala Thr Val Ala Gly Ser Leu Ser Leu Ala Ile Met Met Ala
 530 535 540
 Gly Ile Ser Phe Trp Met Cys Ser Asn Gly Ser Leu Gln Cys Arg Ile
 545 550 555 560
 Cys Ile

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1467 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Influenza virus
- (B) STRAIN: cold-adapted "Master Strain" A/Ann Arbor/6/60 7PI
(H2N2)

(vii) IMMEDIATE SOURCE:

- (B) CLONE: NA

(ix) FEATURE:

- (A) NAME/KEY: mutation
- (B) LOCATION: replace(394, "u")
- (D) OTHER INFORMATION: /product= "Neuraminidase"
/gene= "NA"
/note= "u in ca "master" strain; c in
wt2(3)"
/citation= ([1])

(ix) FEATURE:

- (A) NAME/KEY: mutation
- (B) LOCATION: replace(604, "u")
- (D) OTHER INFORMATION: /product= "Neuraminidase"
/gene= "NA"
/note= "u in ca "master" strain; a in
wt2(3)"
/citation= ([1])

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 20..1426
- (D) OTHER INFORMATION: /product= "neuraminidase"
/gene= "NA"

/note= "neuraminidase protein"
/citation= ([1])

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Herlocher, M L
Maassab, H F
Webster, R G

(B) TITLE: Molecular and biological changes in the cold adapted
master strain A/AA/6/60 (H2N2) Influenza Virus

(C) JOURNAL: Proceedings of the National Academy of Sciences of
the USA

(G) DATE: 1993

(K) RELEVANT RESIDUES IN SEQ ID NO:19: FROM 1 TO 1467

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

AGCAAAAGCA GGAGUGAAA AUG AAU CCA AAU CAA AAG ACA AUA ACA AUU GGC	52
Met Asn Pro Asn Gln Lys Thr Ile Thr Ile Gly	
1 5 10	
UCU GUC UCU CUC ACC AUC GCA ACA GUA UGC UUC CUC AUG CAG AUU GCC	100
Ser Val Ser Leu Thr Ile Ala Thr Val Cys Phe Leu Met Gln Ile Ala	
15 20 25	
AUC CUG GCA ACU ACU GUG ACA UUG CAC CUU AAG CAA CAU GAG UGC GAC	148
Ile Leu Ala Thr Thr Val Thr Leu His Leu Lys Gln His Glu Cys Asp	
30 35 40	
UCC CCC GCG AGC AAC CAA GUA AUG CCA UGU GAA CCA AUA AUA AUA GAA	196
Ser Pro Ala Ser Asn Gln Val Met Pro Cys Glu Pro Ile Ile Ile Glu	
45 50 55	
AGG AAC AUA ACA GAG AUA GUG UAU UUG AAU AAC ACC ACC AUA GAG AAA	244
Arg Asn Ile Thr Glu Ile Val Tyr Leu Asn Asn Thr Thr Ile Glu Lys	
60 65 70 75	
GAG AUU UGC CCC GAA GUA GUG GGA UAC AGA AAU UGG UCA AAG CCG CAA	292
Glu Ile Cys Pro Glu Val Val Gly Tyr Arg Asn Trp Ser Lys Pro Gln	
80 85 90	
UGU CAA AUU ACA GGA UUU GCA CCU UUU UCU AAG GAC AAU UCA AUC CGG	340
Cys Gln Ile Thr Gly Phe Ala Pro Phe Ser Lys Asp Asn Ser Ile Arg	
95 100 105	
CUU UCU GCU GGU GGG GAC AUU UGG GUG ACG AGA GAA CCU UAU GUG UCA	388
Leu Ser Ala Gly Gly Asp Ile Trp Val Thr Arg Glu Pro Tyr Val Ser	
110 115 120	

UGC Cys 125	GAU Asp	CCU Pro	GGC Gly	AAG Lys	UGU Cys	UAU Tyr 130	CAA Gln	UUU Phe	GCA Ala	CUC Leu	GGG Gly 135	CAG Gln	GGG Gly	ACC Thr	ACA Thr	436
CUA Leu 140	GAC Asp	AAC Asn	AAA Lys	CAU His	UCA Ser 145	AAU Asn	GGC Gly	ACA Thr	AUA Ile	CAU His 150	GAU Asp	AGA Arg	AUC Ile	CCU Pro	CAU His 155	484
CGA Arg	ACC Thr	CUA Leu	UUA Leu	AUG Met 160	AAU Asn	GAG Glu	UUG Leu	GGU Gly	GUU Val 165	CCA Pro	UUU Phe	CAU His	UUA Leu	GGA Gly 170	ACC Thr	532
AAA Lys	CAA Gln	GUG Val 175	UGU Cys	GCA Ala	GCA Ala	UGG Trp	UCC Ser	AGC Ser 180	UCA Ser	AGU Ser	UGU Cys	CAC His	GAU Asp 185	GGA Gly	AAA Lys	580
GCA Ala	UGG Trp	UUG Leu 190	CAU His	GUU Val	UGU Cys	GUC Val	ACU Thr 195	GGG Gly	GAU Asp	GAU Asp	AGA Arg	AAU Asn 200	GCA Ala	ACU Thr	GCU Ala	628
AGC Ser 205	UUC Phe	AUU Ile	UAU Tyr	GAC Asp	GGG Gly	AAG Lys 210	CUU Leu	GUG Val	GAC Asp	AGU Ser	AUU Ile 215	GGU Gly	UCA Ser	UGG Trp	UCU Ser	676
CAA Gln 220	AAU Asn	GUC Val	CUC Leu	AGG Arg	ACC Thr 225	CAG Gln	GAG Glu	UCG Ser	GAA Glu	UGC Cys 230	GUC Val	UGU Cys	AUC Ile	AAU Asn	GGG Gly 235	724
ACU Thr	UGC Cys	ACA Thr	GUA Val	GUA Val 240	AUG Met	ACU Thr	GAU Asp	GGA Gly	AGU Ser 245	GCA Ala	UCA Ser	GGA Gly	AGA Arg	GCU Ala 250	GAU Asp	772
ACU Thr	AGA Arg	AUA Ile	CUA Leu 255	UUC Phe	AUU Ile	AAA Lys	GAG Glu	GGG Gly 260	AAA Lys	AUU Ile	GUC Val	CAU His	AUU Ile 265	GGC Gly	CCA Pro	820
UUG Leu	UCA Ser	GGA Gly 270	AGU Ser	GCU Ala	CAG Gln	CAU His	GUA Val 275	GAG Glu	GAG Glu	UGU Cys	UCU Ser	UGU Cys 280	UAC Tyr	CCU Pro	CGA Arg	868
UAU Tyr 285	CCU Pro	GAC Asp	GUC Val	AGA Arg	UGU Cys	AUC Ile 290	UGC Cys	AGA Arg	GAC Asp	AAC Asn	UGG Trp 295	AAA Lys	GGC Gly	UCU Ser	AAU Asn	916
AGG Arg 300	CCC Pro	GUU Val	AUA Ile	GAC Asp	AUA Ile 305	AAU Asn	AUG Met	GAA Glu	GAU Asp	UAU Tyr 310	AGC Ser	AUU Ile	GAU Asp	UCC Ser 315	AGU Ser	964
UAU Tyr	GUG Val	UGC Cys	UCA Ser	GGG Gly 320	CUU Leu	GUU Val	GGC Gly	GAC Asp	ACA Thr 325	CCC Pro	AGG Arg	AAC Asn	GAC Asp	GAC Asp 330	AGC Ser	1012
UCU Ser	AGC Ser	AAU Asn	AGC Ser 335	AAU Asn	UGC Cys	AGG Arg	GAU Asp	CCU Pro 340	AAC Asn	AAU Asn	GAG Glu	AGA Arg	GGG Gly 345	AAU Asn	CCA Pro	1060

GGA GUG AAA GGC UGG GCC UUU GAC AAU GGA GAU GAU GUA UGG AUG GGA 1108
 Gly Val Lys Gly Trp Ala Phe Asp Asn Gly Asp Asp Val Trp Met Gly
 350 355 360
 AGA ACA AUC AGC AAA GAU UUA CGC UCA GGU UAU GAA ACU UUC AAA GUC 1156
 Arg Thr Ile Ser Lys Asp Leu Arg Ser Gly Tyr Glu Thr Phe Lys Val
 365 370 375
 AUU GGU GGU UGG UCC ACA CCU AAU UCC AAA UCG CAG GUC AAU AGA CAG 1204
 Ile Gly Gly Trp Ser Thr Pro Asn Ser Lys Ser Gln Val Asn Arg Gln
 380 385 390 395
 GUC AUA GUU GAC AAC AAU AAU UGG UCU GGU UAC UCU GGU AUU UUC UCU 1252
 Val Ile Val Asp Asn Asn Asn Trp Ser Gly Tyr Ser Gly Ile Phe Ser
 400 405 410
 GUU GAG GGC AAA AGC UGC AUC AAU AGG UGC UUU UAU GUG GAG UUG AUA 1300
 Val Glu Gly Lys Ser Cys Ile Asn Arg Cys Phe Tyr Val Glu Leu Ile
 415 420 425
 AGG GGA AGG CCA CAG GAG ACU AGA GUA UGG UGG ACC UCA AAC AGU AUU 1348
 Arg Gly Arg Pro Gln Glu Thr Arg Val Trp Trp Thr Ser Asn Ser Ile
 430 435 440
 GUU GUA UUU UGU GGC ACU UCA GGU ACU UAU GGA ACA GGC UCA UGG CCU 1396
 Val Val Phe Cys Gly Thr Ser Gly Thr Tyr Gly Thr Gly Ser Trp Pro
 445 450 455
 GAU GGG GCG AAC AUC AAU UUC AUG CCU AUA UAACGUUUCG CAAUUUUAGA 1446
 Asp Gly Ala Asn Ile Asn Phe Met Pro Ile
 460 465
 AAAAAACUCC UUGUUUCUAC U 1467

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 469 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Met Asn Pro Asn Gln Lys Thr Ile Thr Ile Gly Ser Val Ser Leu Thr
 1 5 10 15

Ile Ala Thr Val Cys Phe Leu Met Gln Ile Ala Ile Leu Ala Thr Thr
 20 25 30
 Val Thr Leu His Leu Lys Gln His Glu Cys Asp Ser Pro Ala Ser Asn
 35 40 45
 Gln Val Met Pro Cys Glu Pro Ile Ile Ile Glu Arg Asn Ile Thr Glu
 50 55 60
 Ile Val Tyr Leu Asn Asn Thr Thr Ile Glu Lys Glu Ile Cys Pro Glu
 65 70 75 80
 Val Val Gly Tyr Arg Asn Trp Ser Lys Pro Gln Cys Gln Ile Thr Gly
 85 90 95
 Phe Ala Pro Phe Ser Lys Asp Asn Ser Ile Arg Leu Ser Ala Gly Gly
 100 105 110
 Asp Ile Trp Val Thr Arg Glu Pro Tyr Val Ser Cys Asp Pro Gly Lys
 115 120 125
 Cys Tyr Gln Phe Ala Leu Gly Gln Gly Thr Thr Leu Asp Asn Lys His
 130 135 140
 Ser Asn Gly Thr Ile His Asp Arg Ile Pro His Arg Thr Leu Leu Met
 145 150 155 160
 Asn Glu Leu Gly Val Pro Phe His Leu Gly Thr Lys Gln Val Cys Ala
 165 170 175
 Ala Trp Ser Ser Ser Ser Cys His Asp Gly Lys Ala Trp Leu His Val
 180 185 190
 Cys Val Thr Gly Asp Asp Arg Asn Ala Thr Ala Ser Phe Ile Tyr Asp
 195 200 205
 Gly Lys Leu Val Asp Ser Ile Gly Ser Trp Ser Gln Asn Val Leu Arg
 210 215 220
 Thr Gln Glu Ser Glu Cys Val Cys Ile Asn Gly Thr Cys Thr Val Val
 225 230 235 240
 Met Thr Asp Gly Ser Ala Ser Gly Arg Ala Asp Thr Arg Ile Leu Phe
 245 250 255
 Ile Lys Glu Gly Lys Ile Val His Ile Gly Pro Leu Ser Gly Ser Ala
 260 265 270
 Gln His Val Glu Glu Cys Ser Cys Tyr Pro Arg Tyr Pro Asp Val Arg
 275 280 285
 Cys Ile Cys Arg Asp Asn Trp Lys Gly Ser Asn Arg Pro Val Ile Asp
 290 295 300
 Ile Asn Met Glu Asp Tyr Ser Ile Asp Ser Ser Tyr Val Cys Ser Gly

(2) INFORMATION FOR SEQ ID NO:21:

(A) LENGTH: 890 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Influenza virus

(B) STRAIN: wild type A/Ann Arbor/6/60 (H2N2) Egg Passage 2(3)

61
(vii) IMMEDIATE SOURCE:

(B) CLONE: NS

(ix) FEATURE:

(A) NAME/KEY: exon

(B) LOCATION: 27..56

(D) OTHER INFORMATION: /product= "nonstructural protein NS2"
/gene= "NS"
/note= "nonstructural protein NS2"
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: conflict

(B) LOCATION: replace(483, "a")

(D) OTHER INFORMATION: /note= "a in ca "master" strain and in
wt2(3); g in 1988 reported wild type
E28-32 strain"
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: exon

(B) LOCATION: 529..861

(D) OTHER INFORMATION: /product= "nonstructural protein NS2"
/gene= "NS"
/note= "nonstructural protein NS2"
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: conflict

(B) LOCATION: replace(813, "g")

(D) OTHER INFORMATION: /note= "g in ca "master" strain and in
wt2(3); a in 1988 reported wild type
E28-32 strain"
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: join(27..56, 529..861)

(D) OTHER INFORMATION: /product= "nonstructural protein NS2"
/gene= "NS"
/note= "nonstructural protein NS2"
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 27..677

(D) OTHER INFORMATION: /product= "nonstructural protein NS1"
/gene= "NS"
/note= "nonstructural protein NS1"
/citation= ([1][2])

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Herlocher, M L
Maassab, H F
Webster, R G

(B) TITLE: Molecular and biological changes in the cold adapted
master strain A/AA/6/60 (H2N2) influenza virus

(C) JOURNAL: Proceedings of the National Academy of Sciences of
the USA

(G) DATE: 1993

(K) RELEVANT RESIDUES IN SEQ ID NO:21: FROM 1 TO 890

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Cox, N J
Kitame, F
Kendal, A P
Maassab, H F
Naeve, C

(B) TITLE: Identification of sequence changes in the cold-adapted
live attenuated influenza vaccine strain, A/Ann
Arbor/6/60(H2N2)

(C) JOURNAL: Virology

(D) VOLUME: 167

(F) PAGES: 554-567

(G) DATE: 1988

(K) RELEVANT RESIDUES IN SEQ ID NO:21: FROM 1 TO 890

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

AGCAAAAGCA GGGUGACAAA GACAU	AUG GAU CCU AAC ACU GUG UCA AGC UUU	53
	Met Asp Pro Asn Thr Val Ser Ser Phe	
	1 5	
CAG GUA GAU UGC UUC CUU UGG CAU GUC CGC AAA CAA GUU GCA GAC CAA		101
Gln Val Asp Cys Phe Leu Trp His Val Arg Lys Gln Val Ala Asp Gln		
10 15 20 25		
GAA CUA GGU GAU GCC CCA UUC CUU GAU CGG CUU CGC CGA GAU CAG AAG		149
Glu Leu Gly Asp Ala Pro Phe Leu Asp Arg Leu Arg Arg Asp Gln Lys		
	30 35 40	
UCC CUA AGG GGA AGA GGC AGU ACU CUC GGU CUG AAC AUC GAA ACA GCC		197
Ser Leu Arg Gly Arg Gly Ser Thr Leu Gly Leu Asn Ile Glu Thr Ala		
	45 50 55	
ACC CGU GUU GGA AAG CAG AUA GUG GAG AGG AUU CUG AAG GAA GAA UCC		245
Thr Arg Val Gly Lys Gln Ile Val Glu Arg Ile Leu Lys Glu Glu Ser		
	60 65 70	
GAU GAG GCA CUU AAA AUG ACC AUG GCC UCC GCA CCU GCU UCG CGA UAC		293
Asp Glu Ala Leu Lys Met Thr Met Ala Ser Ala Pro Ala Ser Arg Tyr		
	75 80 85	
CUA ACU GAC AUG ACU AUU GAG GAA AUG UCA AGG GAC UGG UUC AUG CUA		341
Leu Thr Asp Met Thr Ile Glu Glu Met Ser Arg Asp Trp Phe Met Leu		
	90 95 100 105	
AUG CCC AAG CAG AAA GUG GCA GGC CCU CUU UGU AUC AGA AUG GAC CAG		389
Met Pro Lys Gln Lys Val Ala Gly Pro Leu Cys Ile Arg Met Asp Gln		
	110 115 120	
GCA AUC AUG GAU AAG AAC AUC AUA UUG AAA GCG AAU UUC AGU GUG AUU		437
Ala Ile Met Asp Lys Asn Ile Ile Leu Lys Ala Asn Phe Ser Val Ile		
	125 130 135	
UUU GAC CGG CUA GAG ACC CUA AUA UUA CUA AGG GCU UUC ACC GAA ACG		485
Phe Asp Arg Leu Glu Thr Leu Ile Leu Leu Arg Ala Phe Thr Glu Thr		
	140 145 150	
GGA GCA AUU GUU GGC GAA AUU UCA CCA UUG CCU UCU CUU CCA GGA CAU		533
Gly Ala Ile Val Gly Glu Ile Ser Pro Leu Pro Ser Leu Pro Gly His		
	155 160 165	
ACU AAU GAG GAU GUC AAA AAU GCA AUU GGG GUC CUC AUC GGA GGA CUU		581
Thr Asn Glu Asp Val Lys Asn Ala Ile Gly Val Leu Ile Gly Gly Leu		
	170 175 180 185	
GAA UGG AAU GAU AAC ACA GUU CGA GUC UCU AAA ACU CUA CAG AGA UUC		629
Glu Trp Asn Asp Asn Thr Val Arg Val Ser Lys Thr Leu Gln Arg Phe		

190	195	200	
GCU UGG AGA AGC AGU GAU GAG AAU GGG AGA CCU CCA CUC ACU CCA AAA			677
Ala Trp Arg Ser Ser Asp Glu Asn Gly Arg Pro Pro Leu Thr Pro Lys			
205	210	215	
UAGAAACGGA AAAUGGCGAG AACAAUUAGG UCAAAAAGUUC GAAGAAUAA GAUGGCUGAU			737
UGAAGAAGUG AGACACAAAU UGAAGAUAA AGAGAAUAGU UUUGAGCAAA UAACAUUUUAU			797
GCAAGCCUUA CAGCUGCUAU UUGAAGUGGA ACAAGAGAU AGAACUUUCU CGUUUCAGCU			857
UAUUUAAUGA UAAAAAACAC CCUUGUUUCU ACU			890

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 217 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Met	Asp	Pro	Asn	Thr	Val	Ser	Ser	Phe	Gln	Val	Asp	Cys	Phe	Leu	Trp
1				5					10					15	
His	Val	Arg	Lys	Gln	Val	Ala	Asp	Gln	Glu	Leu	Gly	Asp	Ala	Pro	Phe
			20					25					30		
Leu	Asp	Arg	Leu	Arg	Arg	Asp	Gln	Lys	Ser	Leu	Arg	Gly	Arg	Gly	Ser
		35					40					45			
Thr	Leu	Gly	Leu	Asn	Ile	Glu	Thr	Ala	Thr	Arg	Val	Gly	Lys	Gln	Ile
	50					55					60				
Val	Glu	Arg	Ile	Leu	Lys	Glu	Glu	Ser	Asp	Glu	Ala	Leu	Lys	Met	Thr
65				70					75					80	
Met	Ala	Ser	Ala	Pro	Ala	Ser	Arg	Tyr	Leu	Thr	Asp	Met	Thr	Ile	Glu
			85						90					95	
Glu	Met	Ser	Arg	Asp	Trp	Phe	Met	Leu	Met	Pro	Lys	Gln	Lys	Val	Ala
			100					105					110		
Gly	Pro	Leu	Cys	Ile	Arg	Met	Asp	Gln	Ala	Ile	Met	Asp	Lys	Asn	Ile
		115					120					125			

Ile Leu Lys Ala Asn Phe Ser Val Ile Phe Asp Arg Leu Glu Thr Leu
 130 135 140

Ile Leu Leu Arg Ala Phe Thr Glu Thr Gly Ala Ile Val Gly Glu Ile
 145 150 155 160

Ser Pro Leu Pro Ser Leu Pro Gly His Thr Asn Glu Asp Val Lys Asn
 165 170 175

Ala Ile Gly Val Leu Ile Gly Gly Leu Glu Trp Asn Asp Asn Thr Val
 180 185 190

Arg Val Ser Lys Thr Leu Gln Arg Phe Ala Trp Arg Ser Ser Asp Glu
 195 200 205

Asn Gly Arg Pro Pro Leu Thr Pro Lys
 210 215

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 418 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 27..389
- (D) OTHER INFORMATION: /product= "Nonstructural protein 2"
 /gene= "NS2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

AGCAAAAGCA GGGUGACAAA GACAU	AUG GAU CCU AAC ACU GUG UCA AGC UUU	53
	Met Asp Pro Asn Thr Val Ser Ser Phe	
	1 5	
CAG GAC AUA CUA AUG AGG AUG UCA AAA AUG CAA UUG GGG UCC UCA UCG		101
Gln Asp Ile Leu Met Arg Met Ser Lys Met Gln Leu Gly Ser Ser Ser		
10 15 20 25		
GAG GAC UUG AAU GGA AUG AUA ACA CAG UUC GAG UCU CUA AAA CUC UAC		149

Glu	Asp	Leu	Asn	Gly	Met	Ile	Thr	Gln	Phe	Glu	Ser	Leu	Lys	Leu	Tyr		
				30					35					40			
AGA	GAU	UCG	CUU	GGA	GAA	GCA	GUG	AUG	AGA	AUG	GGA	GAC	CUC	CAC	UCA	197	
Arg	Asp	Ser	Leu	Gly	Glu	Ala	Val	Met	Arg	Met	Gly	Asp	Leu	His	Ser		
			45					50					55				
CUC	CAA	AAU	AGA	AAC	GGA	AAA	UGG	CGA	GAA	CAA	UUA	GGU	CAA	AAG	UUC	245	
Leu	Gln	Asn	Arg	Asn	Gly	Lys	Trp	Arg	Glu	Gln	Leu	Gly	Gln	Lys	Phe		
		60					65					70					
GAA	GAA	AUA	AGA	UGG	CUG	AUU	GAA	GAA	GUG	AGA	CAC	AAA	UUG	AAG	AUA	293	
Glu	Glu	Ile	Arg	Trp	Leu	Ile	Glu	Glu	Val	Arg	His	Lys	Leu	Lys	Ile		
	75					80					85						
ACA	GAG	AAU	AGU	UUU	GAG	CAA	AUA	ACA	UUU	AUG	CAA	GCC	UUA	CAG	CUG	341	
Thr	Glu	Asn	Ser	Phe	Glu	Gln	Ile	Thr	Phe	Met	Gln	Ala	Leu	Gln	Leu		
	90				95					100					105		
CUA	UUU	GAA	GUG	GAA	CAA	GAG	AUA	AGA	ACU	UUC	UCG	UUU	CAG	CUU	AUU	389	
Leu	Phe	Glu	Val	Glu	Gln	Glu	Ile	Arg	Thr	Phe	Ser	Phe	Gln	Leu	Ile		
				110					115					120			
UAAUGAUAAA AAACACCCUU GUUUCUACU																418	

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 121 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Met	Asp	Pro	Asn	Thr	Val	Ser	Ser	Phe	Gln	Asp	Ile	Leu	Met	Arg	Met		
1				5					10					15			
Ser	Lys	Met	Gln	Leu	Gly	Ser	Ser	Ser	Glu	Asp	Leu	Asn	Gly	Met	Ile		
		20						25					30				
Thr	Gln	Phe	Glu	Ser	Leu	Lys	Leu	Tyr	Arg	Asp	Ser	Leu	Gly	Glu	Ala		
		35					40					45					
Val	Met	Arg	Met	Gly	Asp	Leu	His	Ser	Leu	Gln	Asn	Arg	Asn	Gly	Lys		
	50					55					60						
Trp	Arg	Glu	Gln	Leu	Gly	Gln	Lys	Phe	Glu	Glu	Ile	Arg	Trp	Leu	Ile		

65 70 75 80
Glu Glu Val Arg His Lys Leu Lys Ile Thr Glu Asn Ser Phe Glu Gln
 85 90 95
Ile Thr Phe Met Gln Ala Leu Gln Leu Leu Phe Glu Val Glu Gln Glu
 100 105 110
Ile Arg Thr Phe Ser Phe Gln Leu Ile
 115 120

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1027 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Influenza virus
- (B) STRAIN: wild type A/Ann Arbor/6/60 (H2N2) Egg Passage 2(3)

(vii) IMMEDIATE SOURCE:

- (B) CLONE: M

(ix) FEATURE:

- (A) NAME/KEY: exon
- (B) LOCATION: 26..51
- (D) OTHER INFORMATION: /product= "matrix protein M2"
/gene= "M"
/note= "matrix protein M2"
/citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: exon

(B) LOCATION: 740..1004

(D) OTHER INFORMATION: /product= "matrix protein M2"
/gene= "M"
/note= "matrix protein M2"
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: conflict

(B) LOCATION: replace(969, "u")

(D) OTHER INFORMATION: /note= "u in ca "master" strain and in
wt2(3); g in 1988 reported wild type
E28-32 strain"
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: join(26..51, 740..1004)

(D) OTHER INFORMATION: /product= "matrix protein M2"
/gene= "M"
/note= "matrix protein M2"
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 26..781

(D) OTHER INFORMATION: /product= "matrix protein M1"
/gene= "M"
/note= "matrix protein M1"
/citation= ([1][2])

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Herlocher, M L
Maassab, H F
Webster, R G

(B) TITLE: Molecular and biological changes in the cold adapted
master strain A/AA/6/60 (H2N2) influenza virus

(C) JOURNAL: Proceedings of the National Academy of Sciences of
the USA

(G) DATE: 1993

(K) RELEVANT RESIDUES IN SEQ ID NO:25: FROM 1 TO 1027

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Cox, N J
Kitame, F
Kendal, A P
Maassab, H F
Naeve, C

(B) TITLE: Identification of sequence changes in the cold-adapted
live attenuated influenza vaccine strain, A/Ann
Arbor/6/60(H2N2)

(C) JOURNAL: Virology

(D) VOLUME: 167

(F) PAGES: 554-557

(G) DATE: 1988

(K) RELEVANT RESIDUES IN SEQ ID NO:25: FROM 1 TO 1027

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

AGCAAAAGCA GGUAGAUUU GAAAG AUG AGU CUU CUA ACC GAG GUC GAA ACG	52
Met Ser Leu Leu Thr Glu Val Glu Thr	
1 5	
UAC GUU CUC UCU AUC AUC CCG UCA GGC CCC CUC AAA GCC GAG AUC GCA	100
Tyr Val Leu Ser Ile Ile Pro Ser Gly Pro Leu Lys Ala Glu Ile Ala	
10 15 20 25	
CAG AGA CUU GAA GAU GUC UUU GCU GGG AAA AAC ACC GAU CUU GAG GCU	148
Gln Arg Leu Glu Asp Val Phe Ala Gly Lys Asn Thr Asp Leu Glu Ala	
30 35 40	
CUC AUG GAA UGG CUA AAG ACA AGA CCA AUC CUG UCA CCU CUG ACU AAG	196
Leu Met Glu Trp Leu Lys Thr Arg Pro Ile Leu Ser Pro Leu Thr Lys	
45 50 55	
GGG AUU UUG GGA UUU GUA UUC ACG CUC ACC GUG CCC AGU GAG CGA GGA	244
Gly Ile Leu Gly Phe Val Phe Thr Leu Thr Val Pro Ser Glu Arg Gly	
60 65 70	
CUG CAG CGU AGA CGC UUU GUC CAA AAU GCC CUC AAU GGG AAU GGG GAU	292
Leu Gln Arg Arg Arg Phe Val Gln Asn Ala Leu Asn Gly Asn Gly Asp	
75 80 85	
CCA AAU AAC AUG GAC AGA GCA GUU AAA CUG UAU AGA AAG CUU AAG AGG	340

Pro 90	Asn	Asn	Met	Asp	Arg 95	Ala	Val	Lys	Leu	Tyr 100	Arg	Lys	Leu	Lys	Arg 105	
GAG	AUA	ACA	UUC	CAU	GGG	GCC	AAA	GAA	AUA	GCG	CUC	AGU	UAU	UCU	GCU	388
Glu	Ile	Thr	Phe	His	Gly	Ala	Lys	Glu	Ile	Ala	Leu	Ser	Tyr	Ser	Ala	
				110					115					120		
GGU	GCA	CUU	GCC	AGU	UGU	AUG	GGC	CUC	AUA	UAC	AAC	AGG	AUG	GGG	GCU	436
Gly	Ala	Leu	Ala	Ser	Cys	Met	Gly	Leu	Ile	Tyr	Asn	Arg	Met	Gly	Ala	
			125					130					135			
GUG	ACC	ACU	GAA	GUG	GUC	UUA	GGC	CUG	GUA	UGU	GCA	ACC	UGU	GAA	CAG	484
Val	Thr	Thr	Glu	Val	Val	Leu	Gly	Leu	Val	Cys	Ala	Thr	Cys	Glu	Gln	
			140				145						150			
AUU	GCU	GAC	UCC	CAG	CAU	AGG	UCU	CAU	AGG	CAA	AUG	GUG	ACA	ACA	ACC	532
Ile	Ala	Asp	Ser	Gln	His	Arg	Ser	His	Arg	Gln	Met	Val	Thr	Thr	Thr	
	155					160					165					
AAU	CCA	CUA	AUA	AGA	CAU	GAG	AAC	AGA	AUG	GUU	CUG	GCC	AGC	ACU	ACA	580
Asn	Pro	Leu	Ile	Arg	His	Glu	Asn	Arg	Met	Val	Leu	Ala	Ser	Thr	Thr	
170					175					180					185	
GCU	AAG	GCU	AUG	GAG	CAA	AUG	GCU	GGA	UCG	AGU	GAG	CAA	GCA	GCA	GAG	628
Ala	Lys	Ala	Met	Glu	Gln	Met	Ala	Gly	Ser	Ser	Glu	Gln	Ala	Ala	Glu	
				190					195					200		
GCC	AUG	GAG	GUU	GCU	AGU	CAG	GCC	AGG	CAA	AUG	GUG	CAG	GCA	AUG	AGA	676
Ala	Met	Glu	Val	Ala	Ser	Gln	Ala	Arg	Gln	Met	Val	Gln	Ala	Met	Arg	
			205					210					215			
GUU	AUU	GGG	ACU	CAU	CCU	AGC	UCC	AGU	GCU	GGU	CUA	AAA	AAU	GAU	CUU	724
Val	Ile	Gly	Thr	His	Pro	Ser	Ser	Ser	Ala	Gly	Leu	Lys	Asn	Asp	Leu	
		220					225					230				
CUU	GAA	AAU	UUG	CAG	GCC	UAU	CAG	AAA	CGA	AUG	GGG	GUG	CAG	AUG	CAA	772
Leu	Glu	Asn	Leu	Gln	Ala	Tyr	Gln	Lys	Arg	Met	Gly	Val	Gln	Met	Gln	
	235					240					245					
CGA	UUC	AAG	UGACCCUCUU	GUUGUUGCCG	CGAGUAUCAU	UGGGAUCUUG										821
Arg	Phe	Lys														
250																
CACUUGAUAU	UGUGGAUUCU	UGAUCAUCUU	UUUUUCAAU	GCAUUUAUCG	CUUCUUUAAA											881
CACGGUCUGA	AAAGAGGGCC	UUCUACGGAA	GGAGUACCAG	AGUCUAUGAG	GGAAGAAUUA											941
CGAAAGGAAC	AGCAGAGUGC	UGUGGAUUCU	GACGAUAGUC	AUUUUGUCAG	CAUAGAGCUG											1001
GAGUAAAAA	CUACCUUGUU	UCUACU														1027

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 252 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Met Ser Leu Leu Thr Glu Val Glu Thr Tyr Val Leu Ser Ile Ile Pro
1 5 10 15
Ser Gly Pro Leu Lys Ala Glu Ile Ala Gln Arg Leu Glu Asp Val Phe
20 25 30
Ala Gly Lys Asn Thr Asp Leu Glu Ala Leu Met Glu Trp Leu Lys Thr
35 40 45
Arg Pro Ile Leu Ser Pro Leu Thr Lys Gly Ile Leu Gly Phe Val Phe
50 55 60
Thr Leu Thr Val Pro Ser Glu Arg Gly Leu Gln Arg Arg Arg Phe Val
65 70 75 80
Gln Asn Ala Leu Asn Gly Asn Gly Asp Pro Asn Asn Met Asp Arg Ala
85 90 95
Val Lys Leu Tyr Arg Lys Leu Lys Arg Glu Ile Thr Phe His Gly Ala
100 105 110
Lys Glu Ile Ala Leu Ser Tyr Ser Ala Gly Ala Leu Ala Ser Cys Met
115 120 125
Gly Leu Ile Tyr Asn Arg Met Gly Ala Val Thr Thr Glu Val Val Leu
130 135 140
Gly Leu Val Cys Ala Thr Cys Glu Gln Ile Ala Asp Ser Gln His Arg
145 150 155 160
Ser His Arg Gln Met Val Thr Thr Thr Asn Pro Leu Ile Arg His Glu
165 170 175
Asn Arg Met Val Leu Ala Ser Thr Thr Ala Lys Ala Met Glu Gln Met
180 185 190
Ala Gly Ser Ser Glu Gln Ala Ala Glu Ala Met Glu Val Ala Ser Gln
195 200 205
Ala Arg Gln Met Val Gln Ala Met Arg Val Ile Gly Thr His Pro Ser
210 215 220

Ser Ser Ala Gly Leu Lys Asn Asp Leu Leu Glu Asn Leu Gln Ala Tyr
225 230 235 240

Gln Lys Arg Met Gly Val Gln Met Gln Arg Phe Lys
245 250

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 339 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 26..316

(D) OTHER INFORMATION: /product= "Matrix M2"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

AGCAAAAGCA GGUAGAUUU GAAAG AUG AGU CUU CUA ACC GAG GUC GAA ACG	52
Met Ser Leu Leu Thr Glu Val Glu Thr	
1 5	
CCU AUC AGA AAC GAA UGG GGG UGC AGA UGC AAC GAU UCA AGU GAC CCU	100
Pro Ile Arg Asn Glu Trp Gly Cys Arg Cys Asn Asp Ser Ser Asp Pro	
10 15 20 25	
CUU GUU GUU GCC GCG AGU AUC AUU GGG AUC UUG CAC UUG AUA UUG UGG	148
Leu Val Val Ala Ala Ser Ile Ile Gly Ile Leu His Leu Ile Leu Trp	
30 35 40	
AUU CUU GAU CAU CUU UUU UUC AAA UGC AUU UAU CGC UUC UUU AAA CAC	196
Ile Leu Asp His Leu Phe Phe Lys Cys Ile Tyr Arg Phe Phe Lys His	
45 50 55	
GGU CUG AAA AGA GGG CCU UCU ACG GAA GGA GUA CCA GAG UCU AUG AGG	244
Gly Leu Lys Arg Gly Pro Ser Thr Glu Gly Val Pro Glu Ser Met Arg	
60 65 70	

GAA GAA UAU CGA AAG GAA CAG CAG AGU GCU GUG GAU UCU GAC GAU AGU 292
 Glu Glu Tyr Arg Lys Glu Gln Gln Ser Ala Val Asp Ser Asp Asp Ser
 75 80 85

CAU UUU GUC AGC AUA GAG CUG GAG UAAAAACUA CCUUGUUUCU ACU 339
 His Phe Val Ser Ile Glu Leu Glu
 90 95

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 97 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Met Ser Leu Leu Thr Glu Val Glu Thr Pro Ile Arg Asn Glu Trp Gly
 1 5 10 15
 Cys Arg Cys Asn Asp Ser Ser Asp Pro Leu Val Val Ala Ala Ser Ile
 20 25 30
 Ile Gly Ile Leu His Leu Ile Leu Trp Ile Leu Asp His Leu Phe Phe
 35 40 45
 Lys Cys Ile Tyr Arg Phe Phe Lys His Gly Leu Lys Arg Gly Pro Ser
 50 55 60
 Thr Glu Gly Val Pro Glu Ser Met Arg Glu Glu Tyr Arg Lys Glu Gln
 65 70 75 80
 Gln Ser Ala Val Asp Ser Asp Asp Ser His Phe Val Ser Ile Glu Leu
 85 90 95
 Glu

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2341 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

a
(ii) MOLECULE TYPE: RNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Influenza virus

(B) STRAIN: wild type A/Ann Arbor/6/60 (H2N2) egg passage 2(3)

(vii) IMMEDIATE SOURCE:

(B) CLONE: PB2

(ix) FEATURE:

(A) NAME/KEY: mutation

(B) LOCATION: replace(141, "a")

(D) OTHER INFORMATION: /note= "g in ca "master" strain; a in
wt2(3); a in 1988 reported wild type
E28-32 strain"
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: conflict

(B) LOCATION: replace(426, "c")

(D) OTHER INFORMATION: /note= "c in ca "master" strain and in
wt2(3); u in 1988 reported wild type
E28-32 strain"
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: conflict

(B) LOCATION: replace(714, "u")

(D) OTHER INFORMATION: /note= "u in ca "master" strain and in
wt2(3); c in 1988 reported wild type
E28-32 strain"
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: conflict

(B) LOCATION: replace(821, "g")

(D) OTHER INFORMATION: /note= "g in ca "master" strain and in
wt2(3); a in 1988 reported wild type
E28-32 strain"
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: conflict

(B) LOCATION: replace(963, "g")

(D) OTHER INFORMATION: /note= "g in ca "master" strain and in
wt2(3); a in 1988 reported wild type
E28-32 strain"
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: conflict

(B) LOCATION: replace(1182, "u")

(D) OTHER INFORMATION: /note= "u in ca "master" strain and in
wt2(3); a in 1988 reported wild type
E28-32 strain"
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: conflict

(B) LOCATION: replace(1212, "u")

(D) OTHER INFORMATION: /note= "u in ca "master" strain and in
wt2(3); c in 1988 reported wild type
E28-32 strain"
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: conflict

(B) LOCATION: replace(1353, "g")

(D) OTHER INFORMATION: /note= "g in ca "master" strain and in

wt2(3); u in 1988 reported wild type
E28-32 strain"
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: conflict

(B) LOCATION: replace(1923, "g")

(D) OTHER INFORMATION: /note= "g in ca "master" strain and in
wt2(3); a in 1988 reported wild type
E28-32 strain"
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: mutation

(B) LOCATION: replace(1933, "u")

(D) OTHER INFORMATION: /note= "c in ca "master" strain; u in
wt2(3); u in 1988 reported wild type
E28-32 strain"
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 28..2304

(D) OTHER INFORMATION: /product= "polymerase basic 2"
/gene= "PB2"
/note= "polymerase basic 2"
/citation= ([1][2])

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Herlocher, M L
Maassab, H F
Webster, R G

(B) TITLE: Molecular and biological changes in the cold
adapted master strain A/AA/6/60 (H2N2) influenza virus

(C) JOURNAL: Proceedings of the National Academy of Sciences of
the USA

(G) DATE: 1993

(K) RELEVANT RESIDUES IN SEQ ID NO:29: FROM 1 TO 2341

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Cox, N J
Kitame, F
Kendal, A P
Maassab, H F
Naeve, C

(B) TITLE: Identification of sequence changes in the cold-adapted
live attenuated influenza vaccine strain, A/Ann
Arbor/6/60(H2N2)

(C) JOURNAL: Virology

(D) VOLUME: 167

(F) PAGES: 554-567

(G) DATE: 1988

(K) RELEVANT RESIDUES IN SEQ ID NO:29: FROM 1 TO 2341

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

AGCGAAAGCA	GGUCAUUUAU	AUUCAAU	AUG	GAA	AGA	AUA	AAA	GAA	CUA	CGG	51					
			Met	Glu	Arg	Ile	Lys	Glu	Leu	Arg						
			1				5									
AAU	CUG	AUG	UCG	CAG	UCU	CGC	ACU	CGC	GAG	AUA	CUA	ACA	AAA	ACC	ACA	99
Asn	Leu	Met	Ser	Gln	Ser	Arg	Thr	Arg	Glu	Ile	Leu	Thr	Lys	Thr	Thr	
	10					15					20					
GUG	GAC	CAU	AUG	GCC	AUA	AUU	AAG	AAG	UAC	ACA	UCA	GGG	AGA	CAG	GAA	147
Val	Asp	His	Met	Ala	Ile	Ile	Lys	Lys	Tyr	Thr	Ser	Gly	Arg	Gln	Glu	
	25				30					35					40	
AAG	AAC	CCG	UCA	CUU	AGG	AUG	AAA	UGG	AUG	AUG	GCA	AUG	AAA	UAU	CCG	195
Lys	Asn	Pro	Ser	Leu	Arg	Met	Lys	Trp	Met	Met	Ala	Met	Lys	Tyr	Pro	
				45					50					55		
AUU	ACA	GCC	GAC	AAG	AGG	AUA	ACA	GAA	AUG	AUU	CCU	GAG	AGA	AAU	GAG	243
Ile	Thr	Ala	Asp	Lys	Arg	Ile	Thr	Glu	Met	Ile	Pro	Glu	Arg	Asn	Glu	
		60						65					70			
CAA	GGG	CAA	ACU	CUA	UGG	AGU	AAA	AUG	AGU	GAU	GCC	GGA	UCG	GAU	CGU	291
Gln	Gly	Gln	Thr	Leu	Trp	Ser	Lys	Met	Ser	Asp	Ala	Gly	Ser	Asp	Arg	
		75					80					85				
GUG	AUG	GUA	UCA	CCU	CUG	GCU	GUG	ACA	UGG	UGG	AAU	AGA	AAU	GGA	CCA	339
Val	Met	Val	Ser	Pro	Leu	Ala	Val	Thr	Trp	Trp	Asn	Arg	Asn	Gly	Pro	

	90				95				100							
AUG Met 105	ACA Thr	AGU Ser	ACG Thr	GUU Val	CAU His 110	UAU Tyr	CCA Pro	AAA Lys	AUC Ile	UAC Tyr 115	AAA Lys	ACU Thr	UAU Tyr	UUU Phe	GAG Glu 120	387
AAA Lys	GUC Val	GAA Glu	AGG Arg	UUA Leu 125	AAA Lys	CAU His	GGA Gly	ACC Thr	UUU Phe 130	GGC Gly	CCU Pro	GUC Val	CAU His	UUU Phe 135	AGA Arg	435
AAC Asn	CAA Gln	GUC Val	AAA Lys 140	AUA Ile	CGC Arg	CGA Arg	AGA Arg	GUU Val 145	GAC Asp	AUA Ile	AAU Asn	CCU Pro	GGU Gly 150	CAU His	GCA Ala	483
GAC Asp	CUC Leu	AGU Ser 155	GCC Ala	AAG Lys	GAG Glu	GCA Ala	CAG Gln 160	GAU Asp	GUA Val	AUC Ile	AUG Met	GAA Glu 165	GUU Val	GUU Val	UUC Phe	531
CCU Pro	AAC Asn 170	GAA Glu	GUG Val	GGG Gly	GCC Ala	AGG Arg 175	AUA Ile	CUA Leu	ACG Thr	UCG Ser	GAA Glu 180	UCG Ser	CAA Gln	UUA Leu	ACA Thr	579
AUA Ile 185	ACC Thr	AAA Lys	GAG Glu	AAA Lys	AAA Lys 190	GAA Glu	GAA Glu	CUC Leu	CAG Gln	GAU Asp 195	UGC Cys	AAA Lys	AUU Ile	UCA Ser	CCU Pro 200	627
UUG Leu	AUG Met	GUU Val	GCG Ala	UAC Tyr 205	AUG Met	UUA Leu	GAG Glu	AGA Arg	GAA Glu 210	CUU Leu	GUC Val	CGA Arg	AAA Lys	ACG Thr 215	AGA Arg	675
UUU Phe	CUC Leu	CCA Pro	GUU Val 220	GCU Ala	GGU Gly	GGA Gly	ACA Thr	AGC Ser 225	AGU Ser	GUG Val	UAC Tyr	AUU Ile	GAA Glu 230	GUG Val	UUG Leu	723
CAC His	UUG Leu	ACU Thr 235	CAA Gln	GGA Gly	ACA Thr	UGC Cys	UGG Trp 240	GAA Glu	CAG Gln	AUG Met	UAC Tyr	ACU Thr 245	CCA Pro	GGU Gly	GGA Gly	771
GAA Glu	GUG Val 250	AGG Arg	AAU Asn	GAU Asp	GAU Asp	GUU Val 255	GAU Asp	CAA Gln	AGU Ser	CUA Leu	AUU Ile 260	AUU Ile	GCA Ala	GCC Ala	AGG Arg	819
AGC Ser 265	AUA Ile	GUG Val	AGA Arg	AGA Arg	GCA Ala 270	GCA Ala	GUA Val	UCA Ser	GCA Ala	GAU Asp 275	CCA Pro	CUA Leu	GCA Ala	UCU Ser	UUA Leu 280	867
UUG Leu	GAG Glu	AUG Met	UGC Cys	CAC His 285	AGC Ser	ACA Thr	CAG Gln	AUU Ile	GGC Gly 290	GGG Gly	ACA Thr	AGG Arg	AUG Met	GUG Val 295	GAC Asp	915
AUU Ile	CUU Leu	AGG Arg	CAG Gln 300	AAC Asn	CCA Pro	ACA Thr	GAA Glu	GAG Glu 305	CAA Gln	GCU Ala	GUG Val	GAA Glu	AUA Ile 310	UGC Cys	AAG Lys	963
GCU	GCA	AUG	GGA	CUG	AGG	AUC	AGC	UCA	UCC	UUC	AGU	UUU	GGC	GGG	UUC	1011

Ala	Ala	Met	Gly	Leu	Arg	Ile	Ser	Ser	Ser	Phe	Ser	Phe	Gly	Gly	Phe	
		315					320					325				
ACA	UUU	AAG	AGA	ACA	AGC	GGA	UCA	UCA	GUC	AAG	AGA	GAG	GAA	GAA	GUG	1059
Thr	Phe	Lys	Arg	Thr	Ser	Gly	Ser	Ser	Val	Lys	Arg	Glu	Glu	Glu	Val	
	330					335					340					
CUU	ACG	GGC	AAU	CUU	CAA	ACA	UUG	AAA	AUA	AGG	GUG	CAU	GAG	GGA	UAC	1107
Leu	Thr	Gly	Asn	Leu	Gln	Thr	Leu	Lys	Ile	Arg	Val	His	Glu	Gly	Tyr	
345					350					355					360	
GAG	GAG	UUC	ACA	AUG	GUU	GGG	AAA	AGG	GCA	ACA	GCU	AUA	CUC	AGA	AAA	1155
Glu	Glu	Phe	Thr	Met	Val	Gly	Lys	Arg	Ala	Thr	Ala	Ile	Leu	Arg	Lys	
				365					370					375		
GCA	ACC	AGG	AGA	UUG	AUU	CAG	CUG	AUU	GUG	AGU	GGA	AGA	GAC	GAA	CAG	1203
Ala	Thr	Arg	Arg	Leu	Ile	Gln	Leu	Ile	Val	Ser	Gly	Arg	Asp	Glu	Gln	
			380					385					390			
UCG	AUA	GCU	GAA	GCA	AUA	AUU	GUG	GCC	AUG	GUA	UUU	UCA	CAA	GAA	GAU	1251
Ser	Ile	Ala	Glu	Ala	Ile	Ile	Val	Ala	Met	Val	Phe	Ser	Gln	Glu	Asp	
	395						400					405				
UGU	AUG	AUA	AAA	GCA	GUU	AGA	GGU	GAU	CUG	AAU	UUC	GUU	AAU	AGG	GCA	1299
Cys	Met	Ile	Lys	Ala	Val	Arg	Gly	Asp	Leu	Asn	Phe	Val	Asn	Arg	Ala	
	410					415					420					
AAU	CAG	CGA	UUG	AAU	CCC	AUG	CAU	CAA	CUU	UUA	AGA	CAU	UUU	CAG	AAG	1347
Asn	Gln	Arg	Leu	Asn	Pro	Met	His	Gln	Leu	Leu	Arg	His	Phe	Gln	Lys	
425					430					435					440	
GAU	GCG	AAA	GUG	CUU	UUU	CAA	AAU	UGG	GGA	AUU	GAA	CAU	AUC	GAC	AAU	1395
Asp	Ala	Lys	Val	Leu	Phe	Gln	Asn	Trp	Gly	Ile	Glu	His	Ile	Asp	Asn	
				445					450					455		
GUG	AUG	GGA	AUG	AUU	GGG	GUA	UUA	CCA	GAC	AUG	ACU	CCA	AGC	ACA	GAG	1443
Val	Met	Gly	Met	Ile	Gly	Val	Leu	Pro	Asp	Met	Thr	Pro	Ser	Thr	Glu	
			460					465					470			
AUG	UCA	AUG	AGA	GGG	GUA	AGA	GUC	AGC	AAA	AUG	GGC	GUA	GAU	GAA	UAC	1491
Met	Ser	Met	Arg	Gly	Val	Arg	Val	Ser	Lys	Met	Gly	Val	Asp	Glu	Tyr	
		475					480					485				
UCC	AGC	GCG	GAG	AGA	GUA	GUG	GUG	AGC	AUU	GAC	CGG	UUU	UUG	AGA	GUU	1539
Ser	Ser	Ala	Glu	Arg	Val	Val	Val	Ser	Ile	Asp	Arg	Phe	Leu	Arg	Val	
	490					495					500					
CGA	GAC	CAA	CGA	GGA	AAU	GUA	CUA	CUA	UCU	CCU	GAG	GAG	GUC	AGU	GAA	1587
Arg	Asp	Gln	Arg	Gly	Asn	Val	Leu	Leu	Ser	Pro	Glu	Glu	Val	Ser	Glu	
505					510					515					520	
ACA	CAG	GGA	ACA	GAG	AAA	CUG	ACA	AUA	ACU	UAC	UCA	UCG	UCA	AUG	AUG	1635
Thr	Gln	Gly	Thr	Glu	Lys	Leu	Thr	Ile	Thr	Tyr	Ser	Ser	Ser	Met	Met	
				525					530					535		

UGG	GAG	AUU	AAU	GGC	CCU	GAG	UCA	GUG	UUG	GUC	AAU	ACC	UAU	CAG	UGG	1683
Trp	Glu	Ile	Asn	Gly	Pro	Glu	Ser	Val	Leu	Val	Asn	Thr	Tyr	Gln	Trp	
			540					545					550			
AUC	AUC	AGA	AAC	UGG	GAA	ACU	GUU	AAA	AUU	CAG	UGG	UCU	CAG	AAU	CCU	1731
Ile	Ile	Arg	Asn	Trp	Glu	Thr	Val	Lys	Ile	Gln	Trp	Ser	Gln	Asn	Pro	
		555					560					565				
ACA	AUG	CUA	UAC	AAU	AAA	AUG	GAA	UUU	GAG	CCA	UUU	CAG	UCU	UUA	GUU	1779
Thr	Met	Leu	Tyr	Asn	Lys	Met	Glu	Phe	Glu	Pro	Phe	Gln	Ser	Leu	Val	
	570					575					580					
CCU	AAG	GCC	AUU	AGA	GGC	CAA	UAC	AGU	GGG	UUU	GUU	AGG	ACU	CUA	UUC	1827
Pro	Lys	Ala	Ile	Arg	Gly	Gln	Tyr	Ser	Gly	Phe	Val	Arg	Thr	Leu	Phe	
585					590				595						600	
CAA	CAA	AUG	AGG	GAU	GUA	CUU	GGG	ACA	UUU	GAU	ACC	ACC	CAG	AUA	AUA	1875
Gln	Gln	Met	Arg	Asp	Val	Leu	Gly	Thr	Phe	Asp	Thr	Thr	Gln	Ile	Ile	
				605				610						615		
AAA	CUU	CUU	CCC	UUU	GCA	GCC	GCC	CCA	CCA	AAG	CAA	AGU	AGA	AUG	CAG	1923
Lys	Leu	Leu	Pro	Phe	Ala	Ala	Ala	Pro	Pro	Lys	Gln	Ser	Arg	Met	Gln	
			620					625					630			
UUC	UCU	UCA	UUG	ACU	GUG	AAU	GUG	AGG	GGA	UCA	GGA	AUG	AGA	AUA	CUU	1971
Phe	Ser	Ser	Leu	Thr	Val	Asn	Val	Arg	Gly	Ser	Gly	Met	Arg	Ile	Leu	
		635					640					645				
GUA	AGG	GGC	AAU	UCU	CCU	AUA	UUC	AAC	UAC	AAC	AAG	ACC	ACU	AAG	AGA	2019
Val	Arg	Gly	Asn	Ser	Pro	Ile	Phe	Asn	Tyr	Asn	Lys	Thr	Thr	Lys	Arg	
	650					655					660					
CUA	ACA	AUU	CUC	GGA	AAG	GAU	GCU	GGC	ACU	UUA	ACU	GAA	GAC	CCA	GAU	2067
Leu	Thr	Ile	Leu	Gly	Lys	Asp	Ala	Gly	Thr	Leu	Thr	Glu	Asp	Pro	Asp	
665					670					675					680	
GAA	GGC	ACA	UCU	GGA	GUG	GAG	UCC	GCU	GUU	CUG	AGA	GGA	UUC	CUC	AUU	2115
Glu	Gly	Thr	Ser	Gly	Val	Glu	Ser	Ala	Val	Leu	Arg	Gly	Phe	Leu	Ile	
				685					690					695		
CUG	GGC	AAA	GAA	GAU	AGG	AGA	UAU	GGA	CCA	GCA	UUA	AGC	AUC	AAU	GAA	2163
Leu	Gly	Lys	Glu	Asp	Arg	Arg	Tyr	Gly	Pro	Ala	Leu	Ser	Ile	Asn	Glu	
			700					705					710			
CUG	AGU	AAC	CUU	GCG	AAA	GGA	GAA	AAG	GCU	AAU	GUA	CUA	AUU	GGG	CAA	2211
Leu	Ser	Asn	Leu	Ala	Lys	Gly	Glu	Lys	Ala	Asn	Val	Leu	Ile	Gly	Gln	
		715					720					725				
GGA	GAC	GUG	GUG	UUG	GUA	AUG	AAA	CGA	AAA	CGG	AAC	UCU	AGC	AUA	CUU	2259
Gly	Asp	Val	Val	Leu	Val	Met	Lys	Arg	Lys	Arg	Asn	Ser	Ser	Ile	Leu	
	730					735					740					
ACU	GAC	AGC	CAG	ACA	GCG	ACC	AAA	AGG	AUU	CGG	AUG	GCC	AUC	AAU		2304
Thr	Asp	Ser	Gln	Thr	Ala	Thr	Lys	Arg	Ile	Arg	Met	Ala	Ile	Asn		
745					750					755						

UAAUGUUGAA UAGUUUAAAA ACGACCUUGU UUCUACU

2341

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 759 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Met Glu Arg Ile Lys Glu Leu Arg Asn Leu Met Ser Gln Ser Arg Thr
1 5 10 15
Arg Glu Ile Leu Thr Lys Thr Thr Val Asp His Met Ala Ile Ile Lys
20 25 30
Lys Tyr Thr Ser Gly Arg Gln Glu Lys Asn Pro Ser Leu Arg Met Lys
35 40 45
Trp Met Met Ala Met Lys Tyr Pro Ile Thr Ala Asp Lys Arg Ile Thr
50 55 60
Glu Met Ile Pro Glu Arg Asn Glu Gln Gly Gln Thr Leu Trp Ser Lys
65 70 75 80
Met Ser Asp Ala Gly Ser Asp Arg Val Met Val Ser Pro Leu Ala Val
85 90 95
Thr Trp Trp Asn Arg Asn Gly Pro Met Thr Ser Thr Val His Tyr Pro
100 105 110
Lys Ile Tyr Lys Thr Tyr Phe Glu Lys Val Glu Arg Leu Lys His Gly
115 120 125
Thr Phe Gly Pro Val His Phe Arg Asn Gln Val Lys Ile Arg Arg Arg
130 135 140
Val Asp Ile Asn Pro Gly His Ala Asp Leu Ser Ala Lys Glu Ala Gln
145 150 155 160
Asp Val Ile Met Glu Val Val Phe Pro Asn Glu Val Gly Ala Arg Ile
165 170 175
Leu Thr Ser Glu Ser Gln Leu Thr Ile Thr Lys Glu Lys Lys Glu Glu
180 185 190

Leu Gln Asp Cys Lys Ile Ser Pro Leu Met Val Ala Tyr Met Leu Glu
 195 200 205
 Arg Glu Leu Val Arg Lys Thr Arg Phe Leu Pro Val Ala Gly Gly Thr
 210 215 220
 Ser Ser Val Tyr Ile Glu Val Leu His Leu Thr Gln Gly Thr Cys Trp
 225 230 235 240
 Glu Gln Met Tyr Thr Pro Gly Gly Glu Val Arg Asn Asp Asp Val Asp
 245 250 255
 Gln Ser Leu Ile Ile Ala Ala Arg Ser Ile Val Arg Arg Ala Ala Val
 260 265 270
 Ser Ala Asp Pro Leu Ala Ser Leu Leu Glu Met Cys His Ser Thr Gln
 275 280 285
 Ile Gly Gly Thr Arg Met Val Asp Ile Leu Arg Gln Asn Pro Thr Glu
 290 295 300
 Glu Gln Ala Val Glu Ile Cys Lys Ala Ala Met Gly Leu Arg Ile Ser
 305 310 315 320
 Ser Ser Phe Ser Phe Gly Gly Phe Thr Phe Lys Arg Thr Ser Gly Ser
 325 330 335
 Ser Val Lys Arg Glu Glu Glu Val Leu Thr Gly Asn Leu Gln Thr Leu
 340 345 350
 Lys Ile Arg Val His Glu Gly Tyr Glu Glu Phe Thr Met Val Gly Lys
 355 360 365
 Arg Ala Thr Ala Ile Leu Arg Lys Ala Thr Arg Arg Leu Ile Gln Leu
 370 375 380
 Ile Val Ser Gly Arg Asp Glu Gln Ser Ile Ala Glu Ala Ile Ile Val
 385 390 395 400
 Ala Met Val Phe Ser Gln Glu Asp Cys Met Ile Lys Ala Val Arg Gly
 405 410 415
 Asp Leu Asn Phe Val Asn Arg Ala Asn Gln Arg Leu Asn Pro Met His
 420 425 430
 Gln Leu Leu Arg His Phe Gln Lys Asp Ala Lys Val Leu Phe Gln Asn
 435 440 445
 Trp Gly Ile Glu His Ile Asp Asn Val Met Gly Met Ile Gly Val Leu
 450 455 460
 Pro Asp Met Thr Pro Ser Thr Glu Met Ser Met Arg Gly Val Arg Val
 465 470 475 480
 Ser Lys Met Gly Val Asp Glu Tyr Ser Ser Ala Glu Arg Val Val Val

485 490 495

Ser Ile Asp Arg Phe Leu Arg Val Arg Asp Gln Arg Gly Asn Val Leu
500 505 510

Leu Ser Pro Glu Glu Val Ser Glu Thr Gln Gly Thr Glu Lys Leu Thr
515 520 525

Ile Thr Tyr Ser Ser Ser Met Met Trp Glu Ile Asn Gly Pro Glu Ser
530 535 540

Val Leu Val Asn Thr Tyr Gln Trp Ile Ile Arg Asn Trp Glu Thr Val
545 550 555 560

Lys Ile Gln Trp Ser Gln Asn Pro Thr Met Leu Tyr Asn Lys Met Glu
565 570 575

Phe Glu Pro Phe Gln Ser Leu Val Pro Lys Ala Ile Arg Gly Gln Tyr
580 585 590

Ser Gly Phe Val Arg Thr Leu Phe Gln Gln Met Arg Asp Val Leu Gly
595 600 605

Thr Phe Asp Thr Thr Gln Ile Ile Lys Leu Leu Pro Phe Ala Ala Ala
610 615 620

Pro Pro Lys Gln Ser Arg Met Gln Phe Ser Ser Leu Thr Val Asn Val
625 630 635 640

Arg Gly Ser Gly Met Arg Ile Leu Val Arg Gly Asn Ser Pro Ile Phe
645 650 655

Asn Tyr Asn Lys Thr Thr Lys Arg Leu Thr Ile Leu Gly Lys Asp Ala
660 665 670

Gly Thr Leu Thr Glu Asp Pro Asp Glu Gly Thr Ser Gly Val Glu Ser
675 680 685

Ala Val Leu Arg Gly Phe Leu Ile Leu Gly Lys Glu Asp Arg Arg Tyr
690 695 700

Gly Pro Ala Leu Ser Ile Asn Glu Leu Ser Asn Leu Ala Lys Gly Glu
705 710 715 720

Lys Ala Asn Val Leu Ile Gly Gln Gly Asp Val Val Leu Val Met Lys
725 730 735

Arg Lys Arg Asn Ser Ser Ile Leu Thr Asp Ser Gln Thr Ala Thr Lys
740 745 750

Arg Ile Arg Met Ala Ile Asn
755

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2341 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Influenza virus
- (B) STRAIN: wild type A/Ann Arbor/6/60 (H2N2) Egg Passage 2(3)

(vii) IMMEDIATE SOURCE:

- (B) CLONE: PB1

(ix) FEATURE:

- (A) NAME/KEY: conflict
- (B) LOCATION: replace(123, "g")
- (D) OTHER INFORMATION: /note= "g in ca "master" strain and in
wt2(3); a in 1988 reported wild type
E28-32 strain"
/citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: conflict
- (B) LOCATION: replace(486, "u")
- (D) OTHER INFORMATION: /note= "u in ca "master" strain and in
wt2(3); c in 1988 reported wild type
E28-32 strain"
/citation= ([1][2])

(ix) FEATURE:

- (A) NAME/KEY: conflict
- (B) LOCATION: replace(1195, "g")

(D) OTHER INFORMATION: /note= "g in ca "master" strain and in
wt2(3); a in 1988 reported wild type
E28-32 strain"
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: mutation

(B) LOCATION: replace(1276, "a")

(D) OTHER INFORMATION: /note= "g in ca "master" strain; a in
wt2(3); g in 1988 reported wild type
E28-32 strain"
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: conflict

(B) LOCATION: replace(1395, "u")

(D) OTHER INFORMATION: /note= "u in ca "master" strain and in
wt2(3); g in 1988 reported wild type
E28-32 strain"
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: conflict

(B) LOCATION: replace(1766, "g")

(D) OTHER INFORMATION: /note= "g in ca "master" strain and in
wt2(3); a in 1988 reported wild type
E28-32 strain"
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: conflict

(B) LOCATION: replace(2005, "a")

(D) OTHER INFORMATION: /note= "a in ca "master" strain and in
wt2(3); g in 1988 reported wild type
E28-32 strain"
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: conflict

(B) LOCATION: replace(2019, "u")

(D) OTHER INFORMATION: /note= "u in ca "master" strain and in
wt2(3); c in 1988 reported wild type
E28-32 strain"
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 25..2295

(D) OTHER INFORMATION: /product= "polymerase basic 1"
/gene= "PB1"
/note= "polymerase basic 1"
/citation= ([1][2])

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Herlocher, M L
Maassab, H F
Webster, R G

(B) TITLE: Molecular and biological changes in the cold adapted
master strain A/AA/6/60 (H2N2) influenza virus

(C) JOURNAL: Proceedings of the National Academy of Sciences of
the USA

(G) DATE: 1993

(K) RELEVANT RESIDUES IN SEQ ID NO:31: FROM 1 TO 2341

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Cox, N J
Kitame, F
Kendal, A P
Maassab, H F
Naeve, C

(B) TITLE: Identification of sequence changes in the cold-adapted
live attenuated influenza vaccine strain

(C) JOURNAL: Virology

(D) VOLUME: 167

(F) PAGES: 554-567

(G) DATE: 1988

(K) RELEVANT RESIDUES IN SEQ ID NO:31: FROM 1 TO 2341

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

AGCGAAAGCA GGCAAACCAU UUGA AUG GAU GUC AAU CCG ACC UUA CUU UUC	51
Met Asp Val Asn Pro Thr Leu Leu Phe	
1 5	
UUG AAA GUU CCA GCG CAA AAU GCC AUA AGU ACU ACA UUC CCU UAU ACU	99
Leu Lys Val Pro Ala Gln Asn Ala Ile Ser Thr Thr Phe Pro Tyr Thr	
10 15 20 25	
GGA GAU CCU CCA UAC AGC CAU GGG ACA GGA ACA GGA UAC ACC AUG GAC	147
Gly Asp Pro Pro Tyr Ser His Gly Thr Gly Thr Gly Tyr Thr Met Asp	
30 35 40	
ACA GUC AAC AGA ACA CAU CAA UAU UCA GAA AAG GGG AAG UGG ACA ACA	195
Thr Val Asn Arg Thr His Gln Tyr Ser Glu Lys Gly Lys Trp Thr Thr	
45 50 55	
AAC ACG GAA ACU GGA GCG CAC CAA CUU AAC CCA AUU GAU GGA CCA CUA	243
Asn Thr Glu Thr Gly Ala His Gln Leu Asn Pro Ile Asp Gly Pro Leu	
60 65 70	
CCU GAG GAC AAU GAA CCA AGU GGA UAU GCA CAA ACA GAC UGC GUC CUG	291
Pro Glu Asp Asn Glu Pro Ser Gly Tyr Ala Gln Thr Asp Cys Val Leu	
75 80 85	
GAA GCA AUG GCU UUC CUU GAA GAA UCC CAC CCA GGA AUC UUU GAA AAC	339
Glu Ala Met Ala Phe Leu Glu Glu Ser His Pro Gly Ile Phe Glu Asn	
90 95 100 105	
UCG UGU CUU GAA ACG AUG GAA GUU AUU CAA CAA ACA AGA GUG GAC AAA	387
Ser Cys Leu Glu Thr Met Glu Val Ile Gln Gln Thr Arg Val Asp Lys	
110 115 120	
CUG ACC CAA GGU CGU CAG ACC UAU GAU UGG ACA UUG AAC AGA AAU CAG	435
Leu Thr Gln Gly Arg Gln Thr Tyr Asp Trp Thr Leu Asn Arg Asn Gln	
125 130 135	
CCG GCU GCA ACU GCG CUA GCC AAC ACU AUA GAG GUC UUC AGA UCG AAU	483
Pro Ala Ala Thr Ala Leu Ala Asn Thr Ile Glu Val Phe Arg Ser Asn	
140 145 150	
GGU CUG ACA GCU AAU GAA UCG GGA AGG CUA AUA GAU UUC CUC AAG GAU	531
Gly Leu Thr Ala Asn Glu Ser Gly Arg Leu Ile Asp Phe Leu Lys Asp	
155 160 165	
GUG AUA GAA UCA AUG GAU AAA GAG GAG AUG GAA AUC ACA ACA CAC UUC	579
Val Ile Glu Ser Met Asp Lys Glu Glu Met Glu Ile Thr Thr His Phe	
170 175 180 185	

CAA	AGA	AAA	AGA	AGA	GUA	AGA	GAC	AAC	AUG	ACC	AAG	AAA	AUG	GUC	ACA	627
Gln	Arg	Lys	Arg	Arg	Val	Arg	Asp	Asn	Met	Thr	Lys	Lys	Met	Val	Thr	
				190					195					200		
CAA	CGA	ACA	AUA	GGA	AAG	AAG	AAG	CAA	AGA	UUG	AAC	AAG	AGA	AGC	UAU	675
Gln	Arg	Thr	Ile	Gly	Lys	Lys	Lys	Gln	Arg	Leu	Asn	Lys	Arg	Ser	Tyr	
			205					210					215			
CUA	AUA	AGA	GCA	CUG	ACA	UUG	AAC	ACA	AUG	ACU	AAA	GAU	GCA	GAG	AGA	723
Leu	Ile	Arg	Ala	Leu	Thr	Leu	Asn	Thr	Met	Thr	Lys	Asp	Ala	Glu	Arg	
		220					225					230				
GGU	AAA	UUA	AAG	AGA	AGA	GCA	AUU	GCA	ACA	CCC	GGU	AUG	CAG	AUC	AGA	771
Gly	Lys	Leu	Lys	Arg	Arg	Ala	Ile	Ala	Thr	Pro	Gly	Met	Gln	Ile	Arg	
	235					240					245					
GGG	UUC	GUG	UAC	UUU	GUC	GAA	ACA	CUA	GCG	AGA	AGU	AUU	UGU	GAG	AAG	819
Gly	Phe	Val	Tyr	Phe	Val	Glu	Thr	Leu	Ala	Arg	Ser	Ile	Cys	Glu	Lys	
250					255					260					265	
CUU	GAA	CAG	UCU	GGG	CUU	CCG	GUU	GGA	GGU	AAU	GAA	AAG	AAG	GCU	AAA	867
Leu	Glu	Gln	Ser	Gly	Leu	Pro	Val	Gly	Gly	Asn	Glu	Lys	Lys	Ala	Lys	
				270					275					280		
CUG	GCA	AAU	GUU	GUG	CGA	AAA	AUG	AUG	ACU	AAU	UCA	CAA	GAC	ACA	GAG	915
Leu	Ala	Asn	Val	Val	Arg	Lys	Met	Met	Thr	Asn	Ser	Gln	Asp	Thr	Glu	
			285					290					295			
CUC	UCU	UUC	ACA	AUU	ACU	GGA	GAC	AAU	ACC	AAA	UGG	AAU	GAG	AAU	CAA	963
Leu	Ser	Phe	Thr	Ile	Thr	Gly	Asp	Asn	Thr	Lys	Trp	Asn	Glu	Asn	Gln	
		300					305					310				
AAU	CCU	CGG	AUG	UUC	CUG	GCG	AUG	AUA	ACA	UAC	AUC	ACA	AGA	AAU	CAA	1011
Asn	Pro	Arg	Met	Phe	Leu	Ala	Met	Ile	Thr	Tyr	Ile	Thr	Arg	Asn	Gln	
	315					320					325					
CCU	GAA	UGG	UUU	AGA	AAC	GUC	CUG	AGC	AUC	GCA	CCU	AUA	AUG	UUC	UCA	1059
Pro	Glu	Trp	Phe	Arg	Asn	Val	Leu	Ser	Ile	Ala	Pro	Ile	Met	Phe	Ser	
330					335					340					345	
AAU	AAA	AUG	GCA	AGA	CUA	GGG	AAA	GGA	UAC	AUG	UUC	AAA	AGC	AAG	AGC	1107
Asn	Lys	Met	Ala	Arg	Leu	Gly	Lys	Gly	Tyr	Met	Phe	Lys	Ser	Lys	Ser	
				350					355					360		
AUG	AAG	CUC	CGA	ACA	CAA	AUA	CCA	GCA	GAA	AUG	CUA	GCA	AGU	AUU	GAC	1155
Met	Lys	Leu	Arg	Thr	Gln	Ile	Pro	Ala	Glu	Met	Leu	Ala	Ser	Ile	Asp	
			365					370					375			
CUG	AAA	UAC	UUU	AAU	GAA	UCA	ACA	AGA	AAG	AAA	AUC	GAG	GAA	AUA	AGG	1203
Leu	Lys	Tyr	Phe	Asn	Glu	Ser	Thr	Arg	Lys	Lys	Ile	Glu	Glu	Ile	Arg	
		380					385					390				
CCU	CUC	CUA	AUA	GAU	GGC	ACA	GUC	UCA	UUG	AGU	CCU	GGA	AUG	AUG	AUG	1251
Pro	Leu	Leu	Ile	Asp	Gly	Thr	Val	Ser	Leu	Ser	Pro	Gly	Met	Met	Met	
	395					400					405					

GGC Gly 410	AUG Met	UUC Phe	AAC Asn	AUG Met	CUA Leu 415	AGU Ser	ACA Thr	AUC Ile	UUA Leu	GGA Gly 420	GUC Val	UCA Ser	AUC Ile	CUG Leu	AAU Asn 425	1299
CUU Leu	GGA Gly	CAA Gln	AAG Lys	AAG Lys 430	UAC Tyr	ACC Thr	AAA Lys	ACA Thr	ACA Thr 435	UAC Tyr	UGG Trp	UGG Trp	GAC Asp	GGA Gly 440	CUC Leu	1347
CAA Gln	UCC Ser	UCU Ser	GAU Asp 445	GAC Asp	UUC Phe	GCC Ala	CUC Leu	AUA Ile 450	GUG Val	AAU Asn	GCA Ala	CCA Pro	AAU Asn 455	CAU His	GAU Asp	1395
GGA Gly	AUA Ile	CAA Gln 460	GCA Ala	GGG Gly	GUG Val	GAU Asp	AGA Arg 465	UUC Phe	UAC Tyr	AGA Arg	ACC Thr	UGC Cys 470	AAG Lys	CUA Leu	GUC Val	1443
GGA Gly 475	AUC Ile	AAU Asn	AUG Met	AGC Ser	AAA Lys	AAG Lys 480	AAG Lys	UCC Ser	UAC Tyr	AUA Ile	AAU Asn 485	AGG Arg	ACA Thr	GGG Gly	ACA Thr	1491
UUU Phe 490	GAA Glu	UUC Phe	ACA Thr	AGC Ser	UUU Phe 495	UUC Phe	UAU Tyr	CGC Arg	UAU Tyr	GGA Gly 500	UUU Phe	GUA Val	GCC Ala	AAU Asn	UUU Phe 505	1539
AGC Ser	AUG Met	GAG Glu	CUG Leu	CCC Pro 510	AGC Ser	UUU Phe	GGA Gly	GUG Val	UCU Ser 515	GGA Gly	AUU Ile	AAU Asn	GAA Glu	UCG Ser 520	GCU Ala	1587
GAU Asp	AUG Met	AGC Ser	AUU Ile 525	GGG Gly	GUA Val	ACA Thr	GUG Val	AUA Ile 530	AAG Lys	AAC Asn	AAC Asn	AUG Met	AUA Ile 535	AAC Asn	AAU Asn	1635
GAC Asp	CUU Leu	GGG Gly 540	CCA Pro	GCA Ala	ACA Thr	GCC Ala	CAA Gln 545	CUG Leu	GCU Ala	CUU Leu	CAA Gln 550	CUA Leu	UUC Phe	AUC Ile	AAA Lys	1683
GAC Asp 555	UAC Tyr	AGA Arg	UAU Tyr	ACG Thr	UAC Tyr	CGG Arg 560	UGC Cys	CAC His	AGA Arg	GGA Gly	GAC Asp 565	ACA Thr	CAA Gln	AUU Ile	CAG Gln	1731
ACA Thr 570	AGG Arg	AGA Arg	UCA Ser	UUC Phe	GAG Glu 575	CUA Leu	AAG Lys	AAG Lys	CUG Leu	UGG Trp 580	GGG Gly	CAA Gln	ACC Thr	CGC Arg	UCA Ser 585	1779
AAG Lys	GCA Ala	GGA Gly	CUU Leu	UUG Leu 590	GUU Val	UCG Ser	GAU Asp	GGA Gly	GGA Gly 595	CCA Pro	AAC Asn	UUA Leu	UAC Tyr	AAU Asn 600	AUC Ile	1827
CGG Arg	AAU Asn	CUC Leu	CAC His 605	AUU Ile	CCA Pro	GAA Glu	GUC Val	UGC Cys 610	UUG Leu	AAG Lys	UGG Trp	GAG Glu	CUA Leu 615	AUG Met	GAU Asp	1875
GAA Glu	GAC Asp	UAU Tyr 620	CAG Gln	GGG Gly	AGG Arg	CUU Leu	UGU Cys 625	AAU Asn	CCC Pro	CUG Leu	AAU Asn	CCA Pro 630	UUU Phe	GUC Val	AGU Ser	1923

CAU AAG GAG AUU GAG UCU GUA AAC AAU GCU GUG GUA AUG CCA GCU CAC His Lys Glu Ile Glu Ser Val Asn Asn Ala Val Val Met Pro Ala His 635 640 645	1971
GGU CCA GCC AAG AGC AUG GAA UAU GAU GCU GUU ACU ACU ACA CAC UCU Gly Pro Ala Lys Ser Met Glu Tyr Asp Ala Val Thr Thr Thr His Ser 650 655 660 665	2019
UGG AUC CCU AAG AGG AAC CGC UCC AUU CUC AAC ACA AGC CAA AGG GGA Trp Ile Pro Lys Arg Asn Arg Ser Ile Leu Asn Thr Ser Gln Arg Gly 670 675 680	2067
AUU CUU GAA GAU GAA CAG AUG UAU CAG AAG UGU UGC AAU CUA UUC GAG Ile Leu Glu Asp Glu Gln Met Tyr Gln Lys Cys Cys Asn Leu Phe Glu 685 690 695	2115
AAA UUC UUC CCU AGC AGU UCG UAC AGG AGA CCA GUU GGA AUU UCC AGC Lys Phe Phe Pro Ser Ser Ser Tyr Arg Arg Pro Val Gly Ile Ser Ser 700 705 710	2163
AUG GUG GAG GCC AUG GUG UCU AGG GCC CGG AUU GAU GCA CGG AUU GAC Met Val Glu Ala Met Val Ser Arg Ala Arg Ile Asp Ala Arg Ile Asp 715 720 725	2211
UUC GAG UCU GGA CGG AUU AAG AAA GAG GAG UUC GCU GAG AUC AUG AAG Phe Glu Ser Gly Arg Ile Lys Lys Glu Glu Phe Ala Glu Ile Met Lys 730 735 740 745	2259
AUC UGU UCC ACC AUU GAA GAG CUC AGA CGG CAA AAA UAGUGAAUUU Ile Cys Ser Thr Ile Glu Glu Leu Arg Arg Gln Lys 750 755	2305
AGCUUGUCCU UCAUGAAAAA AUGCCUUGUU UCUACU	2341

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 757 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Met	Asp	Val	Asn	Pro	Thr	Leu	Leu	Phe	Leu	Lys	Val	Pro	Ala	Gln	Asn
1				5					10					15	
Ala	Ile	Ser	Thr	Thr	Phe	Pro	Tyr	Thr	Gly	Asp	Pro	Pro	Tyr	Ser	His

20 25 30

Gly Thr Gly Thr Gly Tyr Thr Met Asp Thr Val Asn Arg Thr His Gln
35 40 45

Tyr Ser Glu Lys Gly Lys Trp Thr Thr Asn Thr Glu Thr Gly Ala His
50 55 60

Gln Leu Asn Pro Ile Asp Gly Pro Leu Pro Glu Asp Asn Glu Pro Ser
65 70 75 80

Gly Tyr Ala Gln Thr Asp Cys Val Leu Glu Ala Met Ala Phe Leu Glu
85 90 95

Glu Ser His Pro Gly Ile Phe Glu Asn Ser Cys Leu Glu Thr Met Glu
100 105 110

Val Ile Gln Gln Thr Arg Val Asp Lys Leu Thr Gln Gly Arg Gln Thr
115 120 125

Tyr Asp Trp Thr Leu Asn Arg Asn Gln Pro Ala Ala Thr Ala Leu Ala
130 135 140

Asn Thr Ile Glu Val Phe Arg Ser Asn Gly Leu Thr Ala Asn Glu Ser
145 150 155 160

Gly Arg Leu Ile Asp Phe Leu Lys Asp Val Ile Glu Ser Met Asp Lys
165 170 175

Glu Glu Met Glu Ile Thr Thr His Phe Gln Arg Lys Arg Arg Val Arg
180 185 190

Asp Asn Met Thr Lys Lys Met Val Thr Gln Arg Thr Ile Gly Lys Lys
195 200 205

Lys Gln Arg Leu Asn Lys Arg Ser Tyr Leu Ile Arg Ala Leu Thr Leu
210 215 220

Asn Thr Met Thr Lys Asp Ala Glu Arg Gly Lys Leu Lys Arg Arg Ala
225 230 235 240

Ile Ala Thr Pro Gly Met Gln Ile Arg Gly Phe Val Tyr Phe Val Glu
245 250 255

Thr Leu Ala Arg Ser Ile Cys Glu Lys Leu Glu Gln Ser Gly Leu Pro
260 265 270

Val Gly Gly Asn Glu Lys Lys Ala Lys Leu Ala Asn Val Val Arg Lys
275 280 285

Met Met Thr Asn Ser Gln Asp Thr Glu Leu Ser Phe Thr Ile Thr Gly
290 295 300

Asp Asn Thr Lys Trp Asn Glu Asn Gln Asn Pro Arg Met Phe Leu Ala
305 310 315 320

Met Ile Thr Tyr Ile Thr Arg Asn Gln Pro Glu Trp Phe Arg Asn Val
 325 330 335
 Leu Ser Ile Ala Pro Ile Met Phe Ser Asn Lys Met Ala Arg Leu Gly
 340 345 350
 Lys Gly Tyr Met Phe Lys Ser Lys Ser Met Lys Leu Arg Thr Gln Ile
 355 360 365
 Pro Ala Glu Met Leu Ala Ser Ile Asp Leu Lys Tyr Phe Asn Glu Ser
 370 375 380
 Thr Arg Lys Lys Ile Glu Glu Ile Arg Pro Leu Leu Ile Asp Gly Thr
 385 390 395 400
 Val Ser Leu Ser Pro Gly Met Met Met Gly Met Phe Asn Met Leu Ser
 405 410 415
 Thr Ile Leu Gly Val Ser Ile Leu Asn Leu Gly Gln Lys Lys Tyr Thr
 420 425 430
 Lys Thr Thr Tyr Trp Trp Asp Gly Leu Gln Ser Ser Asp Asp Phe Ala
 435 440 445
 Leu Ile Val Asn Ala Pro Asn His Asp Gly Ile Gln Ala Gly Val Asp
 450 455 460
 Arg Phe Tyr Arg Thr Cys Lys Leu Val Gly Ile Asn Met Ser Lys Lys
 465 470 475 480
 Lys Ser Tyr Ile Asn Arg Thr Gly Thr Phe Glu Phe Thr Ser Phe Phe
 485 490 495
 Tyr Arg Tyr Gly Phe Val Ala Asn Phe Ser Met Glu Leu Pro Ser Phe
 500 505 510
 Gly Val Ser Gly Ile Asn Glu Ser Ala Asp Met Ser Ile Gly Val Thr
 515 520 525
 Val Ile Lys Asn Asn Met Ile Asn Asn Asp Leu Gly Pro Ala Thr Ala
 530 535 540
 Gln Leu Ala Leu Gln Leu Phe Ile Lys Asp Tyr Arg Tyr Thr Tyr Arg
 545 550 555 560
 Cys His Arg Gly Asp Thr Gln Ile Gln Thr Arg Arg Ser Phe Glu Leu
 565 570 575
 Lys Lys Leu Trp Gly Gln Thr Arg Ser Lys Ala Gly Leu Leu Val Ser
 580 585 590
 Asp Gly Gly Pro Asn Leu Tyr Asn Ile Arg Asn Leu His Ile Pro Glu
 595 600 605
 Val Cys Leu Lys Trp Glu Leu Met Asp Glu Asp Tyr Gln Gly Arg Leu

610 615 620

Cys Asn Pro Leu Asn Pro Phe Val Ser His Lys Glu Ile Glu Ser Val
625 630 635 640

Asn Asn Ala Val Val Met Pro Ala His Gly Pro Ala Lys Ser Met Glu
645 650 655

Tyr Asp Ala Val Thr Thr Thr His Ser Trp Ile Pro Lys Arg Asn Arg
660 665 670

Ser Ile Leu Asn Thr Ser Gln Arg Gly Ile Leu Glu Asp Glu Gln Met
675 680 685

Tyr Gln Lys Cys Cys Asn Leu Phe Glu Lys Phe Phe Pro Ser Ser Ser
690 695 700

Tyr Arg Arg Pro Val Gly Ile Ser Ser Met Val Glu Ala Met Val Ser
705 710 715 720

Arg Ala Arg Ile Asp Ala Arg Ile Asp Phe Glu Ser Gly Arg Ile Lys
725 730 735

Lys Glu Glu Phe Ala Glu Ile Met Lys Ile Cys Ser Thr Ile Glu Glu
740 745 750

Leu Arg Arg Gln Lys
755

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2233 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Influenza virus
- (B) STRAIN: wild type A/Ann Arbor/6/60 (H2N2) Egg Passage 2(3)

(vii) IMMEDIATE SOURCE:

(B) CLONE: PA

a/
(ix) FEATURE:

(A) NAME/KEY: conflict

(B) LOCATION: replace(20, "c")

(D) OTHER INFORMATION: /note= "c in ca "master" strain and in
wt2(3); u in 1988 reported wild type
E28-32 strain"
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: conflict

(B) LOCATION: replace(75, "g")

(D) OTHER INFORMATION: /note= "g in ca "master" strain and in
wt2(3); u in 1988 reported wild type
E28-32 strain"
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: conflict

(B) LOCATION: replace(1861, "g")

(D) OTHER INFORMATION: /note= "g in ca "master" strain and in
wt2(3); a in 1988 reported wild type
E28-32 strain"
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: conflict

(B) LOCATION: replace(2167..2168, "cc")

(D) OTHER INFORMATION: /note= "cc in ca "master" strain and in
wt2(3); uu in 1988 reported wild type
E28-32 strain"
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 25..2172

(D) OTHER INFORMATION: /product= "polymerase acidic protein"
/gene= "PA"
/note= "polymerase acidic protein"
/citation= ([1][2])

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Herlocher, M L
Maassab, H F
Webster, R G

(B) TITLE: Molecular and biological changes in the cold adapted
master strain A/AA/6/60 (H2N2) influenza virus

(C) JOURNAL: Proceedings of the National Academy of Sciences of
the USA

(G) DATE: 1993

(K) RELEVANT RESIDUES IN SEQ ID NO:33: FROM 1 TO 2233

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Cox, N J
Kitame, F
Kendal, A P
Maassab, H F
Naeve, C

(B) TITLE: Identification of sequence changes in the cold-adapted
live attenuated influenza strain, A/Ann
Arbor/6/60(H2N2)

(C) JOURNAL: Virology

(D) VOLUME: 167

(F) PAGES: 554-567

(G) DATE: 1988

(K) RELEVANT RESIDUES IN SEQ ID NO:33: FROM 1 TO 2233

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

AGCGAAAGCA GGUACUGAUC CGAA AUG GAA GAU UUU GUG CGA CAA UGC UUC	51
Met Glu Asp Phe Val Arg Gln Cys Phe	
1 5	
AAU CCG AUG AUU GUC GAG CUU GCG GAA AAA GCA AUG AAA GAG UAU GGA	99

Asn 10	Pro	Met	Ile	Val	Glu 15	Leu	Ala	Glu	Lys	Ala 20	Met	Lys	Glu	Tyr	Gly 25	
GAG Glu	GAU Asp	CUG Leu	AAA Lys	AUC Ile	GAA Glu	ACA Thr	AAC Asn	AAA Lys	UUU Phe	GCA Ala	GCA Ala	AUA Ile	UGC Cys	ACU Thr	CAC His	147
UUG Leu	GAA Glu	GUA Val	UGC Cys	UUC Phe	AUG Met	UAU Tyr	UCA Ser	GAU Asp	UUU Phe	CAU His	UUC Phe	AUC Ile	AAU Asn	GAG Glu	CAA Gln	195
GGC Gly	GAG Glu	UCA Ser	AUA Ile	AUA Ile	GUA Val	GAG Glu	CUU Leu	GAU Asp	GAU Asp	CCA Pro	AAU Asn	GCA Ala	CUU Leu	UUG Leu	AAG Lys	243
CAC His	AGA Arg	UUU Phe	GAA Glu	AUA Ile	AUA Ile	GAG Glu	GGA Gly	AGA Arg	GAU Asp	CGC Arg	ACA Thr	AUG Met	GCC Ala	UGG Trp	ACA Thr	291
GUA Val	GUA Val	AAC Asn	AGU Ser	AUU Ile	UGC Cys	AAC Asn	ACU Thr	ACA Thr	GGA Gly	GCU Ala	GAG Glu	AAA Lys	CCG Pro	AAG Lys	UUU Phe	339
CUG Leu	CCA Pro	GAU Asp	UUG Leu	UAU Tyr	GAU Asp	UAC Tyr	AAG Lys	GAG Glu	AAU Asn	AGA Arg	UUC Phe	AUC Ile	GAG Glu	AUU Ile	GGA Gly	387
GUG Val	ACA Thr	AGG Arg	AGG Arg	GAA Glu	GUC Val	CAC His	AUA Ile	UAC Tyr	UAU Tyr	CUU Leu	GAA Glu	AAG Lys	GCC Ala	AAU Asn	AAA Lys	435
AUU Ile	AAA Lys	UCU Ser	GAG Glu	AAG Lys	ACA Thr	CAC His	AUC Ile	CAC His	AUU Ile	UUC Phe	UCA Ser	UUC Phe	ACU Thr	GGG Gly	GAA Glu	483
GAA Glu	AUG Met	GCC Ala	ACA Thr	AAG Lys	GCC Ala	GAC Asp	UAC Tyr	ACU Thr	CUC Leu	GAU Asp	GAG Glu	GAA Glu	AGC Ser	AGG Arg	GCU Ala	531
AGG Arg	AUC Ile	AAA Lys	ACC Thr	AGA Arg	CUA Leu	UUC Phe	ACC Thr	AUA Ile	AGA Arg	CAA Gln	GAA Glu	AUG Met	GCU Ala	AGC Ser	AGA Arg	579
GGC Gly	CUC Leu	UGG Trp	GAU Asp	UCC Ser	UUU Phe	CAU His	CAG Gln	UCC Ser	GAA Glu	AGA Arg	GGC Gly	GAA Glu	GAA Glu	ACA Thr	AUU Ile	627
GAA Glu	GAA Glu	AGA Arg	UUU Phe	GAA Glu	AUC Ile	ACA Thr	GGG Gly	ACA Thr	AUG Met	CGC Arg	AGG Arg	CUC Leu	GCC Ala	GAC Asp	CAA Gln	675
AGU Ser	CUC Leu	CCG Pro	CCG Pro	AAC Asn	UUC Phe	UCC Ser	UGC Cys	CUU Leu	GAG Glu	AAU Asn	UUU Phe	AGA Arg	GCC Ala	UAU Tyr	GUG Val	723

GAU Asp 235	GGA Gly 235	UUC Phe 235	GAA Glu 235	CCG Pro 235	AAC Asn 235	GGC Gly 240	UAC Tyr 240	AUU Ile 240	GAG Glu 240	GGC Gly 245	AAG Lys 245	CUU Leu 245	UCU Ser 245	CAA Gln 245	AUG Met 245	771
UCC Ser 250	AAA Lys 250	GAA Glu 250	GUA Val 250	AAU Asn 255	GCU Ala 255	AAA Lys 255	AUU Ile 255	GAA Glu 255	CCU Pro 260	UUU Phe 260	CUG Leu 260	AAA Lys 260	ACA Thr 265	ACA Thr 265	CCA Pro 265	819
AGA Arg 270	CCA Pro 270	AUU Ile 270	AGA Arg 270	CUU Leu 270	CCG Pro 270	GAU Asp 270	GGG Gly 275	CCU Pro 275	CCU Pro 275	UGU Cys 275	UCU Ser 275	CAG Gln 280	CGG Arg 280	UCC Ser 280	AAA Lys 280	867
UUC Phe 285	CUG Leu 285	CUG Leu 285	AUG Met 285	GAU Asp 285	GCU Ala 285	UUA Leu 290	AAA Lys 290	UUA Leu 290	AGC Ser 290	AUU Ile 290	GAG Glu 295	GAC Asp 295	CCA Pro 295	AGU Ser 295	CAC His 295	915
GAA Glu 300	GGA Gly 300	GAG Glu 300	GGA Gly 300	AUA Ile 305	CCA Pro 305	CUA Leu 305	UAU Tyr 305	GAU Asp 305	GCG Ala 310	AUC Ile 310	AAG Lys 310	UGU Cys 310	AUG Met 310	AGA Arg 310	ACA Thr 310	963
UUC Phe 315	UUU Phe 315	GGA Gly 315	UGG Trp 315	AAA Lys 320	GAA Glu 320	CCC Pro 320	UAU Tyr 320	GUU Val 320	GUU Val 320	AAA Lys 325	CCA Pro 325	CAC His 325	GAA Glu 325	AAG Lys 325	GGA Gly 325	1011
AUA Ile 330	AAU Asn 330	CCA Pro 330	AAU Asn 335	UAU Tyr 335	CUG Leu 335	CUG Leu 335	UCA Ser 335	UGG Trp 340	AAG Lys 340	CAA Gln 340	GUA Val 340	CUG Leu 340	GCA Ala 345	GAA Glu 345	CUG Leu 345	1059
CAG Gln 350	GAC Asp 350	AUU Ile 350	GAG Glu 350	AAU Asn 350	GAG Glu 350	GAG Glu 350	AAG Lys 355	AUU Ile 355	CCA Pro 355	AGA Arg 355	ACC Thr 360	AAA Lys 360	AAC Asn 360	AUG Met 360	AAG Lys 360	1107
AAA Lys 365	ACG Thr 365	AGU Ser 365	CAG Gln 365	CUA Leu 365	AAG Lys 365	UGG Trp 370	GCA Ala 370	CUU Leu 370	GGU Gly 370	GAG Glu 375	AAC Asn 375	AUG Met 375	GCA Ala 375	CCA Pro 375	GAG Glu 375	1155
AAG Lys 380	GUA Val 380	GAC Asp 380	UUU Phe 380	GAC Asp 385	GAC Asp 385	UGU Cys 385	AGA Arg 385	GAU Asp 385	GUA Val 390	AGC Ser 390	GAU Asp 390	UUG Leu 390	AAG Lys 390	CAA Gln 390	UAU Tyr 390	1203
GAU Asp 395	AGU Ser 395	GAU Asp 395	GAA Glu 395	CCU Pro 400	GAA Glu 400	UUA Leu 400	AGG Arg 400	UCA Ser 405	CUU Leu 405	UCA Ser 405	AGC Ser 405	UGG Trp 405	AUC Ile 410	CAG Gln 410	AAU Asn 410	1251
GAG Glu 410	UUC Phe 410	AAC Asn 415	AAG Lys 415	GCA Ala 415	UGC Cys 415	GAG Glu 415	CUG Leu 420	ACC Thr 420	GAU Asp 420	UCA Ser 420	AUC Ile 425	UGG Trp 425	AUA Ile 425	GAG Glu 425	CUC Leu 425	1299
GAU Asp 430	GAG Glu 430	AUU Ile 430	GGA Gly 430	GAA Glu 430	GAU Asp 435	GUG Val 435	GCU Ala 435	CCA Pro 435	AUU Ile 435	GAA Glu 440	CAC His 440	AUU Ile 440	GCA Ala 440	AGC Ser 440	AUG Met 440	1347
AGA Arg 445	AGG Arg 445	AAU Asn 445	UAC Tyr 445	UUC Phe 445	ACA Thr 445	GCA Ala 450	GAG Glu 450	GUG Val 450	UCU Ser 450	CAU His 450	UGC Cys 450	AGA Arg 455	GCC Ala 455	ACA Thr 455	GAA Glu 455	1395

UAU Tyr	AUA Ile	AUG Met 460	AAG Lys	GGG Gly	GUA Val	UAC Tyr	AUU Ile 465	AAU Asn	ACU Thr	GCC Ala	UUG Leu 470	CUU Leu	AAU Asn	GCA Ala	UCC Ser	1443
UGU Cys 475	GCA Ala	GCA Ala	AUG Met	GAC Asp	GAU Asp	UUC Phe 480	CAA Gln	CUA Leu	AUU Ile	CCC Pro	AUG Met 485	AUA Ile	AGC Ser	AAA Lys	UGU Cys	1491
AGA Arg 490	ACU Thr	AAA Lys	GAG Glu	GGA Gly	AGG Arg 495	CGA Arg	AAG Lys	ACC Thr	AAU Asn	UUA Leu 500	UAU Tyr	GGU Gly	UUC Phe	AUC Ile	AUA Ile 505	1539
AAA Lys	GGA Gly	AGA Arg	UCU Ser	CAC His 510	UUA Leu	AGG Arg	AAU Asn	GAC Asp	ACC Thr 515	GAC Asp	GUG Val	GUA Val	AAC Asn	UUU Phe 520	GUG Val	1587
AGC Ser	AUG Met	GAG Glu	UUU Phe 525	UCU Ser	CUC Leu	ACU Thr	GAC Asp	CCA Pro 530	AGA Arg	CUU Leu	GAG Glu	CCA Pro	CAC His	AAA Lys	UGG Trp	1635
GAG Glu	AAG Lys	UAC Tyr 540	UGU Cys	GUU Val	CUU Leu	GAG Glu	AUA Ile 545	GGA Gly	GAU Asp	AUG Met	CUA Leu	CUA Leu 550	AGA Arg	AGU Ser	GCC Ala	1683
AUA Ile 555	GGC Gly	CAG Gln	GUG Val	UCA Ser	AGG Arg	CCC Pro 560	AUG Met	UUC Phe	UUG Leu	UAU Tyr	GUG Val 565	AGG Arg	ACA Thr	AAU Asn	GGA Gly	1731
ACA Thr 570	UCA Ser	AAG Lys	AUU Ile	AAA Lys	AUG Met 575	AAA Lys	UGG Trp	GGA Gly	AUG Met	GAG Glu 580	AUG Met	AGG Arg	CGU Arg	UGC Cys	CUC Leu 585	1779
CUU Leu	CAG Gln	UCA Ser	CUC Leu	CAA Gln 590	CAA Gln	AUC Ile	GAG Glu	AGU Ser	AUG Met 595	AUU Ile	GAA Glu	GCC Ala	GAG Glu	UCC Ser 600	UCU Ser	1827
GUC Val	AAG Lys	GAG Glu	AAA Lys 605	GAC Asp	AUG Met	ACC Thr	AAA Lys	GAG Glu 610	UUU Phe	UUC Phe	GAG Glu	AAU Asn	AAA Lys 615	UCA Ser	GAA Glu	1875
ACA Thr	UGG Trp	CCC Pro 620	AUU Ile	GGA Gly	GAG Glu	UCC Ser	CCC Pro 625	AAA Lys	GGA Gly	GUG Val	GAA Glu	GAA Glu 630	GGU Gly	UCC Ser	AUU Ile	1923
GGG Gly 635	AAG Lys	GUC Val	UGC Cys	AGG Arg	ACU Thr	UUA Leu 640	UUA Leu	GCC Ala	AAG Lys	UCG Ser	GUA Val 645	UUC Phe	AAU Asn	AGC Ser	CUG Leu	1971
UAU Tyr 650	GCA Ala	UCU Ser	CCA Pro	CAA Gln	UUA Leu 655	GAA Glu	GGA Gly	UUU Phe	UCA Ser	GCU Ala 660	GAA Glu	UCA Ser	AGA Arg	AAA Lys	CUG Leu 665	2019
CUU Leu	CUU Leu	GUC Val	GUU Val	CAG Gln 670	GCU Ala	CUU Leu	AGG Arg	GAC Asp	AAU Asn 675	CUU Leu	GAA Glu	CCU Pro	GGG Gly	ACC Thr 680	UUU Phe	2067

GAU CUU GGG GGG CUA UAU GAA GCA AUU GAG GAG UGC CUG AUU AAU GAU 2115
 Asp Leu Gly Gly Leu Tyr Glu Ala Ile Glu Glu Cys Leu Ile Asn Asp
 685 690 695

CCC UGG GUU UUG CUU AAU GCG UCU UGG UUC AAC UCC UUC CUA ACA CAU 2163
 Pro Trp Val Leu Leu Asn Ala Ser Trp Phe Asn Ser Phe Leu Thr His
 700 705 710

GCA CCA AGA UAGUUGUGGC AAUGCUACUA UUUGCUAUCC AUACUGUCCA 2212
 Ala Pro Arg
 715

AAAAAGUACC UUGUUUCUAC U 2233

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 716 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Met Glu Asp Phe Val Arg Gln Cys Phe Asn Pro Met Ile Val Glu Leu
 1 5 10 15

Ala Glu Lys Ala Met Lys Glu Tyr Gly Glu Asp Leu Lys Ile Glu Thr
 20 25 30

Asn Lys Phe Ala Ala Ile Cys Thr His Leu Glu Val Cys Phe Met Tyr
 35 40 45

Ser Asp Phe His Phe Ile Asn Glu Gln Gly Glu Ser Ile Ile Val Glu
 50 55 60

Leu Asp Asp Pro Asn Ala Leu Leu Lys His Arg Phe Glu Ile Ile Glu
 65 70 75 80

Gly Arg Asp Arg Thr Met Ala Trp Thr Val Val Asn Ser Ile Cys Asn
 85 90 95

Thr Thr Gly Ala Glu Lys Pro Lys Phe Leu Pro Asp Leu Tyr Asp Tyr
 100 105 110

Lys Glu Asn Arg Phe Ile Glu Ile Gly Val Thr Arg Arg Glu Val His
 115 120 125

Ile Tyr Tyr Leu Glu Lys Ala Asn Lys Ile Lys Ser Glu Lys Thr His
 130 135 140
 Ile His Ile Phe Ser Phe Thr Gly Glu Glu Met Ala Thr Lys Ala Asp
 145 150 155 160
 Tyr Thr Leu Asp Glu Glu Ser Arg Ala Arg Ile Lys Thr Arg Leu Phe
 165 170 175
 Thr Ile Arg Gln Glu Met Ala Ser Arg Gly Leu Trp Asp Ser Phe His
 180 185 190
 Gln Ser Glu Arg Gly Glu Glu Thr Ile Glu Glu Arg Phe Glu Ile Thr
 195 200 205
 Gly Thr Met Arg Arg Leu Ala Asp Gln Ser Leu Pro Pro Asn Phe Ser
 210 215 220
 Cys Leu Glu Asn Phe Arg Ala Tyr Val Asp Gly Phe Glu Pro Asn Gly
 225 230 235 240
 Tyr Ile Glu Gly Lys Leu Ser Gln Met Ser Lys Glu Val Asn Ala Lys
 245 250 255
 Ile Glu Pro Phe Leu Lys Thr Thr Pro Arg Pro Ile Arg Leu Pro Asp
 260 265 270
 Gly Pro Pro Cys Ser Gln Arg Ser Lys Phe Leu Leu Met Asp Ala Leu
 275 280 285
 Lys Leu Ser Ile Glu Asp Pro Ser His Glu Gly Glu Gly Ile Pro Leu
 290 295 300
 Tyr Asp Ala Ile Lys Cys Met Arg Thr Phe Phe Gly Trp Lys Glu Pro
 305 310 315 320
 Tyr Val Val Lys Pro His Glu Lys Gly Ile Asn Pro Asn Tyr Leu Leu
 325 330 335
 Ser Trp Lys Gln Val Leu Ala Glu Leu Gln Asp Ile Glu Asn Glu Glu
 340 345 350
 Lys Ile Pro Arg Thr Lys Asn Met Lys Lys Thr Ser Gln Leu Lys Trp
 355 360 365
 Ala Leu Gly Glu Asn Met Ala Pro Glu Lys Val Asp Phe Asp Asp Cys
 370 375 380
 Arg Asp Val Ser Asp Leu Lys Gln Tyr Asp Ser Asp Glu Pro Glu Leu
 385 390 395 400
 Arg Ser Leu Ser Ser Trp Ile Gln Asn Glu Phe Asn Lys Ala Cys Glu
 405 410 415
 Leu Thr Asp Ser Ile Trp Ile Glu Leu Asp Glu Ile Gly Glu Asp Val

420 425 430
 Ala Pro Ile Glu His Ile Ala Ser Met Arg Arg Asn Tyr Phe Thr Ala
 435 440 445
 Glu Val Ser His Cys Arg Ala Thr Glu Tyr Ile Met Lys Gly Val Tyr
 450 455 460
 Ile Asn Thr Ala Leu Leu Asn Ala Ser Cys Ala Ala Met Asp Asp Phe
 465 470 475 480
 Gln Leu Ile Pro Met Ile Ser Lys Cys Arg Thr Lys Glu Gly Arg Arg
 485 490 495
 Lys Thr Asn Leu Tyr Gly Phe Ile Ile Lys Gly Arg Ser His Leu Arg
 500 505 510
 Asn Asp Thr Asp Val Val Asn Phe Val Ser Met Glu Phe Ser Leu Thr
 515 520 525
 Asp Pro Arg Leu Glu Pro His Lys Trp Glu Lys Tyr Cys Val Leu Glu
 530 535 540
 Ile Gly Asp Met Leu Leu Arg Ser Ala Ile Gly Gln Val Ser Arg Pro
 545 550 555 560
 Met Phe Leu Tyr Val Arg Thr Asn Gly Thr Ser Lys Ile Lys Met Lys
 565 570 575
 Trp Gly Met Glu Met Arg Arg Cys Leu Leu Gln Ser Leu Gln Gln Ile
 580 585 590
 Glu Ser Met Ile Glu Ala Glu Ser Ser Val Lys Glu Lys Asp Met Thr
 595 600 605
 Lys Glu Phe Phe Glu Asn Lys Ser Glu Thr Trp Pro Ile Gly Glu Ser
 610 615 620
 Pro Lys Gly Val Glu Glu Gly Ser Ile Gly Lys Val Cys Arg Thr Leu
 625 630 635 640
 Leu Ala Lys Ser Val Phe Asn Ser Leu Tyr Ala Ser Pro Gln Leu Glu
 645 650 655
 Gly Phe Ser Ala Glu Ser Arg Lys Leu Leu Leu Val Val Gln Ala Leu
 660 665 670
 Arg Asp Asn Leu Glu Pro Gly Thr Phe Asp Leu Gly Gly Leu Tyr Glu
 675 680 685
 Ala Ile Glu Glu Cys Leu Ile Asn Asp Pro Trp Val Leu Leu Asn Ala
 690 695 700
 Ser Trp Phe Asn Ser Phe Leu Thr His Ala Pro Arg
 705 710 715

u1
(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1773 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Influenza virus

(B) STRAIN: wild type A/Ann Arbor/6/60 (H2N2) Egg Passage 2(3)

(vii) IMMEDIATE SOURCE:

(B) CLONE: HA

(ix) FEATURE:

(A) NAME/KEY: mutation

(B) LOCATION: replace(144, "a")

(D) OTHER INFORMATION: /gene= "HA"
/note= "u in ca "master" strain; a in
wt2(3)"
/citation= ([1])

(ix) FEATURE:

(A) NAME/KEY: mutation

(B) LOCATION: replace(455, "g")

(D) OTHER INFORMATION: /gene= "HA"
/note= "a in ca "master" strain; g in
wt2(3)"
/citation= ([1])

(ix) FEATURE:

(A) NAME/KEY: mutation

(B) LOCATION: replace(729, "a")

(D) OTHER INFORMATION: /gene= "HA"
/note= "c in ca "master" strain; a in
wt2(3)"
/citation= ([1])

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 44..1729

(D) OTHER INFORMATION: /product= "hemagglutinin"
/gene= "HA"
/note= "hemagglutinin protein"
/citation= ([1])

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Herlocher, M L
Maassab, H F
Webster, R G

(B) TITLE: Molecular and biological changes in the cold adapted
master strain A/AA/6/60 (H2N2) influenza virus

(C) JOURNAL: Proceedings of the National Academy of Sciences of
the USA

(G) DATE: 1993

(K) RELEVANT RESIDUES IN SEQ ID NO:35: FROM 1 TO 1773

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

AGCAAAAGCA GGGGUUAUAC CAUAGACAAC CAAAAGCAAA ACA AUG GCC AUC AUU	55
Met Ala Ile Ile	
1	
UAU CUC AUU CUC CUG UUC ACA GCA GUG AGA GGG GAC AAG AUA UGC AUU	103
Tyr Leu Ile Leu Leu Phe Thr Ala Val Arg Gly Asp Lys Ile Cys Ile	
5 10 15 20	
GGA UAC CAU GCC AAU AAU UCC ACA GAG ACG GUC GAC ACA AAU CUA GAG	151
Gly Tyr His Ala Asn Asn Ser Thr Glu Thr Val Asp Thr Asn Leu Glu	
25 30 35	
CGG AAC GUC ACU GUG ACU CAU GCC AAG GAC AUU CUU GAG AAG ACC CAU	199
Arg Asn Val Thr Val Thr His Ala Lys Asp Ile Leu Glu Lys Thr His	
40 45 50	

AAC Asn	GGA Gly	AAG Lys 55	UUA Leu	UGC Cys	AAA Lys	CUA Leu	AAC Asn 60	GGA Gly	AUC Ile	CCU Pro	CCA Pro	CUU Leu 65	GAA Glu	CUA Leu	GGG Gly	247
GAC Asp	UGU Cys 70	AGC Ser	AUU Ile	GCC Ala	GGA Gly	UGG Trp 75	CUC Leu	CUU Leu	GGA Gly	AAU Asn	CCA Pro 80	GAA Glu	UGU Cys	GAU Asp	AGG Arg	295
CUU Leu 85	CUA Leu	AGU Ser	GUG Val	CCA Pro	GAA Glu 90	UGG Trp	UCC Ser	UAU Tyr	AUA Ile	AUG Met 95	GAG Glu	AAA Lys	GAA Glu	AAC Asn	CCG Pro 100	343
AGA Arg	AAC Asn	GGU Gly	UUG Leu	UGU Cys 105	UAU Tyr	CCA Pro	GGC Gly	AAC Asn	UUC Phe 110	AAU Asn	GAU Asp	UAU Tyr	GAA Glu	GAA Glu 115	UUG Leu	391
AAA Lys	CAU His	CUC Leu 120	CUC Leu	AGC Ser	AGC Ser	GUG Val	AAA Lys	CAU His 125	UUC Phe	GAG Glu	AAA Lys	GUA Val	AAG Lys 130	AUU Ile	CUG Leu	439
CCC Pro	AAA Lys	GAU Asp 135	AGA Arg	UGG Trp	GCA Ala	CAG Gln	CAU His 140	ACA Thr	ACA Thr	ACU Thr	GGA Gly	GGU Gly 145	UCA Ser	CAG Gln	GCC Ala	487
UGC Cys 150	GCG Ala	GUG Val	UCU Ser	GGU Gly	AAU Asn	CCA Pro 155	UCA Ser	UUC Phe	UUC Phe	AGG Arg	AAC Asn 160	AUG Met	GUC Val	UGG Trp	CUG Leu	535
ACA Thr 165	GAG Glu	GAA Glu	GGA Gly	UCA Ser	AAU Asn 170	UAU Tyr	CCG Pro	GUU Val	GCC Ala	AAA Lys 175	GGA Gly	UCG Ser	UAC Tyr	AAC Asn	AAU Asn 180	583
ACA Thr	AGC Ser	GGA Gly	GAA Glu	CAA Gln 185	AUG Met	CUA Leu	AUA Ile	AUU Ile	UGG Trp 190	GGG Gly	GUG Val	CAC His	CAU His	CCC Pro 195	AUU Ile	631
GAU Asp	GAG Glu	ACA Thr	GAA Glu 200	CAA Gln	AGA Arg	ACA Thr	UUG Leu	UAC Tyr 205	CAG Gln	AAU Asn	GUG Val	GGA Gly	ACC Thr 210	UAU Tyr	GUU Val	679
UCC Ser	GUA Val	GGC Gly 215	ACA Thr	UCA Ser	ACA Thr	UUG Leu	AAC Asn 220	AAA Lys	AGG Arg	UCA Ser	ACC Thr	CCA Pro 225	GAA Glu	AUA Ile	GCA Ala	727
AAA Lys 230	AGG Arg	CCU Pro	AAA Lys	GUG Val	AAU Asn	GGA Gly 235	CUA Leu	GGA Gly	AGU Ser	AGA Arg	AUG Met 240	GAA Glu	UUC Phe	UCU Ser	UGG Trp	775
ACC Thr 245	CUC Leu	UUG Leu	GAU Asp	AUG Met	UGG Trp 250	GAC Asp	ACC Thr	AUA Ile	AAU Asn	UUU Phe 255	GAG Glu	AGU Ser	ACU Thr	GGU Gly	AAU Asn 260	823
CUA Leu	AUU Ile	GCA Ala	CCA Pro	GAG Glu 265	UAU Tyr	GGA Gly	UUC Phe	AAA Lys	AUA Ile 270	UCG Ser	AAA Lys	AGA Arg	GGU Gly	AGU Ser	UCU Ser	871

GGG Gly	AUC Ile	AUG Met	AAA Lys 280	ACA Thr	GAA Glu	GGA Gly	ACA Thr	CUU Leu 285	GAG Glu	AAC Asn	UGU Cys	GAG Glu	ACC Thr 290	AAA Lys	UGC Cys	919
CAA Gln	ACU Thr	CCU Pro 295	UUG Leu	GGA Gly	GCA Ala	AUA Ile	AAU Asn 300	ACA Thr	ACA Thr	UUG Leu	CCU Pro	UUU Phe 305	CAC His	AAU Asn	GUC Val	967
CAC His	CCA Pro 310	CUG Leu	ACA Thr	AUA Ile	GGU Gly	GAG Glu 315	UGC Cys	CCC Pro	AAA Lys	UAU Tyr	GUA Val 320	AAA Lys	UCG Ser	GAG Glu	AAG Lys	1015
UUG Leu 325	GUC Val	UUA Leu	GCA Ala	ACA Thr	GGA Gly 330	CUA Leu	AGG Arg	AAU Asn	GUU Val	CCC Pro 335	CAG Gln	AUU Ile	GAA Glu	UCA Ser	AGA Arg 340	1063
GGA Gly	UUG Leu	UUU Phe	GGG Gly 345	GCA Ala	AUA Ile	GCU Ala	GGU Gly	UUU Phe 350	AUA Ile	GAA Glu	GGA Gly	GGA Gly	UGG Trp	CAA Gln 355	GGA Gly	1111
AUG Met	GUU Val	GAU Asp	GGU Gly 360	UGG Trp	UAU Tyr	GGA Gly	UAC Tyr	CAU His 365	CAC His	AGC Ser	AAU Asn	GAC Asp	CAG Gln 370	GGA Gly	UCA Ser	1159
GGG Gly	UAU Tyr	GCA Ala 375	GCA Ala	GAC Asp	AAA Lys	GAA Glu	UCC Ser 380	ACU Thr	CAA Gln	AAG Lys	GCA Ala	UUU Phe 385	GAU Asp	GGA Gly	AUC Ile	1207
ACC Thr	AAC Asn 390	AAG Lys	GUA Val	AAU Asn	UCU Ser	GUG Val 395	AUU Ile	GAA Glu	AAG Lys	AUA Ile	AAC Asn 400	ACC Thr	CAA Gln	UUU Phe	GAA Glu	1255
GCU Ala 405	GUU Val	GGG Gly	AAA Lys	GAA Glu	UUC Phe 410	AGU Ser	AAC Asn	UUA Leu	GAG Glu	AGA Arg 415	AGA Arg	CUG Leu	GAG Glu	AAC Asn	UUG Leu 420	1303
AAC Asn	AAA Lys	AAG Lys	AUG Met 425	GAA Glu	GAC Asp	GGG Gly	UUU Phe	CUA Leu 430	GAU Asp	GUG Val	UGG Trp	ACA Thr	UAC Tyr	AAU Asn 435	GCU Ala	1351
GAG Glu	CUU Leu	CUA Leu	GUU Val 440	CUG Leu	AUG Met	GAA Glu	AAU Asn	GAG Glu 445	AGG Arg	ACA Thr	CUU Leu	GAC Asp	UUU Phe 450	CAU His	GAU Asp	1399
UCU Ser	AAU Asn	GUC Val 455	AAG Lys	AAU Asn	CUG Leu	UAU Tyr	GAU Asp 460	AAA Lys	GUC Val	AGA Arg	AUG Met	CAG Gln 465	CUG Leu	AGG Arg	GAC Asp	1447
AAC Asn	GUC Val 470	AAA Lys	GAA Glu	CUA Leu	GGA Gly	AAU Asn 475	GGA Gly	UGU Cys	UUU Phe	GAA Glu	UUU Phe 480	UAU Tyr	CAC His	AAA Lys	UGU Cys	1495
GAU Asp 485	GAU Asp	GAA Glu	UGC Cys	AUG Met	AAU Asn 490	AGU Ser	GUG Val	AAA Lys	AAC Asn	GGG Gly 495	ACA Thr	UAU Tyr	GAU Asp	UAU Tyr	CCC Pro 500	1543

AAG UAU GAA GAA GAG UCU AAA CUA AAU AGA AAU GAA AUU AAA GGG GUA	1591
Lys Tyr Glu Glu Glu Ser Lys Leu Asn Arg Asn Glu Ile Lys Gly Val	
505 510 515	
AAA UUG AGC AGC AUG GGG GUU UGU CGG AUC CUU GCC AUU UAU GCU ACA	1639
Lys Leu Ser Ser Met Gly Val Cys Arg Ile Leu Ala Ile Tyr Ala Thr	
520 525 530	
GUA GCA GGU UCU CUG UCA CUG GCA AUC AUG AUG GCU GGG AUC UCU UUC	1687
Val Ala Gly Ser Leu Ser Leu Ala Ile Met Met Ala Gly Ile Ser Phe	
535 540 545	
UGG AUG UGC UCC AAC GGG UCU CUG CAG UGC AGG AUC UGC AUA	1729
Trp Met Cys Ser Asn Gly Ser Leu Gln Cys Arg Ile Cys Ile	
550 555 560	
UGAUUAUAAG UCAUUUUUAUA AUUAAAAACA CCCUUGUUUC UACU	1773

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 562 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Met	Ala	Ile	Ile	Tyr	Leu	Ile	Leu	Leu	Phe	Thr	Ala	Val	Arg	Gly	Asp
1				5					10					15	
Lys	Ile	Cys	Ile	Gly	Tyr	His	Ala	Asn	Asn	Ser	Thr	Glu	Thr	Val	Asp
		20						25					30		
Thr	Asn	Leu	Glu	Arg	Asn	Val	Thr	Val	Thr	His	Ala	Lys	Asp	Ile	Leu
		35					40					45			
Glu	Lys	Thr	His	Asn	Gly	Lys	Leu	Cys	Lys	Leu	Asn	Gly	Ile	Pro	Pro
	50					55					60				
Leu	Glu	Leu	Gly	Asp	Cys	Ser	Ile	Ala	Gly	Trp	Leu	Leu	Gly	Asn	Pro
65				70					75					80	
Glu	Cys	Asp	Arg	Leu	Leu	Ser	Val	Pro	Glu	Trp	Ser	Tyr	Ile	Met	Glu
			85						90					95	
Lys	Glu	Asn	Pro	Arg	Asn	Gly	Leu	Cys	Tyr	Pro	Gly	Asn	Phe	Asn	Asp
		100						105					110		

a/

Tyr	Glu	Glu	Leu	Lys	His	Leu	Leu	Ser	Ser	Val	Lys	His	Phe	Glu	Lys	
		115					120					125				
Val	Lys	Ile	Leu	Pro	Lys	Asp	Arg	Trp	Ala	Gln	His	Thr	Thr	Thr	Gly	
	130					135					140					
Gly	Ser	Gln	Ala	Cys	Ala	Val	Ser	Gly	Asn	Pro	Ser	Phe	Phe	Arg	Asn	
145					150					155					160	
Met	Val	Trp	Leu	Thr	Glu	Glu	Gly	Ser	Asn	Tyr	Pro	Val	Ala	Lys	Gly	
				165					170					175		
Ser	Tyr	Asn	Asn	Thr	Ser	Gly	Glu	Gln	Met	Leu	Ile	Ile	Trp	Gly	Val	
			180					185					190			
His	His	Pro	Ile	Asp	Glu	Thr	Glu	Gln	Arg	Thr	Leu	Tyr	Gln	Asn	Val	
		195					200					205				
Gly	Thr	Tyr	Val	Ser	Val	Gly	Thr	Ser	Thr	Leu	Asn	Lys	Arg	Ser	Thr	
	210					215					220					
Pro	Glu	Ile	Ala	Lys	Arg	Pro	Lys	Val	Asn	Gly	Leu	Gly	Ser	Arg	Met	
225					230					235					240	
Glu	Phe	Ser	Trp	Thr	Leu	Leu	Asp	Met	Trp	Asp	Thr	Ile	Asn	Phe	Glu	
				245					250					255		
Ser	Thr	Gly	Asn	Leu	Ile	Ala	Pro	Glu	Tyr	Gly	Phe	Lys	Ile	Ser	Lys	
			260					265					270			
Arg	Gly	Ser	Ser	Gly	Ile	Met	Lys	Thr	Glu	Gly	Thr	Leu	Glu	Asn	Cys	
		275					280					285				
Glu	Thr	Lys	Cys	Gln	Thr	Pro	Leu	Gly	Ala	Ile	Asn	Thr	Thr	Leu	Pro	
	290					295					300					
Phe	His	Asn	Val	His	Pro	Leu	Thr	Ile	Gly	Glu	Cys	Pro	Lys	Tyr	Val	
305					310					315					320	
Lys	Ser	Glu	Lys	Leu	Val	Leu	Ala	Thr	Gly	Leu	Arg	Asn	Val	Pro	Gln	
				325					330					335		
Ile	Glu	Ser	Arg	Gly	Leu	Phe	Gly	Ala	Ile	Ala	Gly	Phe	Ile	Glu	Gly	
			340					345					350			
Gly	Trp	Gln	Gly	Met	Val	Asp	Gly	Trp	Tyr	Gly	Tyr	His	His	Ser	Asn	
		355					360					365				
Asp	Gln	Gly	Ser	Gly	Tyr	Ala	Ala	Asp	Lys	Glu	Ser	Thr	Gln	Lys	Ala	
	370					375					380					
Phe	Asp	Gly	Ile	Thr	Asn	Lys	Val	Asn	Ser	Val	Ile	Glu	Lys	Ile	Asn	
385					390					395					400	
Thr	Gln	Phe	Glu	Ala	Val	Gly	Lys	Glu	Phe	Ser	Asn	Leu	Glu	Arg	Arg	

405 410 415
 Leu Glu Asn Leu Asn Lys Lys Met Glu Asp Gly Phe Leu Asp Val Trp
 420 425 430
 Thr Tyr Asn Ala Glu Leu Leu Val Leu Met Glu Asn Glu Arg Thr Leu
 435 440 445
 Asp Phe His Asp Ser Asn Val Lys Asn Leu Tyr Asp Lys Val Arg Met
 450 455 460
 Gln Leu Arg Asp Asn Val Lys Glu Leu Gly Asn Gly Cys Phe Glu Phe
 465 470 475 480
 Tyr His Lys Cys Asp Asp Glu Cys Met Asn Ser Val Lys Asn Gly Thr
 485 490 495
 Tyr Asp Tyr Pro Lys Tyr Glu Glu Glu Ser Lys Leu Asn Arg Asn Glu
 500 505 510
 Ile Lys Gly Val Lys Leu Ser Ser Met Gly Val Cys Arg Ile Leu Ala
 515 520 525
 Ile Tyr Ala Thr Val Ala Gly Ser Leu Ser Leu Ala Ile Met Met Ala
 530 535 540
 Gly Ile Ser Phe Trp Met Cys Ser Asn Gly Ser Leu Gln Cys Arg Ile
 545 550 555 560
 Cys Ile

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1467 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Influenza virus
- (B) STRAIN: wild type A/Ann Arbor/6/60 (H2N2) Egg Passage 2(3)

(vii) IMMEDIATE SOURCE:

(B) CLONE: NA

61
(ix) FEATURE:

(A) NAME/KEY: mutation

(B) LOCATION: replace(394, "c")

(D) OTHER INFORMATION: /product= "Neuraminidase"
/gene= "NA"
/note= "u in ca "master" strain; c in
wt2(3)"
/citation= ([1])

(ix) FEATURE:

(A) NAME/KEY: mutation

(B) LOCATION: replace(604, "a")

(D) OTHER INFORMATION: /product= "Neuraminidase"
/gene= "NA"
/note= "u in ca "master" strain; a in
wt2(3)"
/citation= ([1])

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 20..1426

(D) OTHER INFORMATION: /product= "neuraminidase"
/gene= "NA"
/note= "neuraminidase protein"
/citation= ([1])

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Herlocher, M L
Maassab, H F
Webster, R G

(B) TITLE: Molecular and biological changes in the cold adapted
master strain A/AA/6/60 (H2N2) Influenza Virus

(C) JOURNAL: Proceedings of the National Academy of Sciences of
the USA

(G) DATE: 1993.

(K) RELEVANT RESIDUES IN SEQ ID NO:37: FROM 1 TO 1467

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

AGCAAAAGCA GGAGUGAAA AUG AAU CCA AAU CAA AAG ACA AUA ACA AUU GGC	52
Met Asn Pro Asn Gln Lys Thr Ile Thr Ile Gly	
1 5 10	
UCU GUC UCU CUC ACC AUC GCA ACA GUA UGC UUC CUC AUG CAG AUU GCC	100
Ser Val Ser Leu Thr Ile Ala Thr Val Cys Phe Leu Met Gln Ile Ala	
15 20 25	
AUC CUG GCA ACU ACU GUG ACA UUG CAC CUU AAG CAA CAU GAG UGC GAC	148
Ile Leu Ala Thr Thr Val Thr Leu His Leu Lys Gln His Glu Cys Asp	
30 35 40	
UCC CCC GCG AGC AAC CAA GUA AUG CCA UGU GAA CCA AUA AUA AUA GAA	196
Ser Pro Ala Ser Asn Gln Val Met Pro Cys Glu Pro Ile Ile Ile Glu	
45 50 55	
AGG AAC AUA ACA GAG AUA GUG UAU UUG AAU AAC ACC ACC AUA GAG AAA	244
Arg Asn Ile Thr Glu Ile Val Tyr Leu Asn Asn Thr Thr Ile Glu Lys	
60 65 70 75	
GAG AUU UGC CCC GAA GUA GUG GGA UAC AGA AAU UGG UCA AAG CCG CAA	292
Glu Ile Cys Pro Glu Val Val Gly Tyr Arg Asn Trp Ser Lys Pro Gln	
80 85 90	
UGU CAA AUU ACA GGA UUU GCA CCU UUU UCU AAG GAC AAU UCA AUC CGG	340
Cys Gln Ile Thr Gly Phe Ala Pro Phe Ser Lys Asp Asn Ser Ile Arg	
95 100 105	
CUU UCU GCU GGU GGG GAC AUU UGG GUG ACG AGA GAA CCU UAU GUG UCA	388
Leu Ser Ala Gly Gly Asp Ile Trp Val Thr Arg Glu Pro Tyr Val Ser	
110 115 120	
UGC GAC CCU GGC AAG UGU UAU CAA UUU GCA CUC GGG CAG GGG ACC ACA	436
Cys Asp Pro Gly Lys Cys Tyr Gln Phe Ala Leu Gly Gln Gly Thr Thr	
125 130 135	
CUA GAC AAC AAA CAU UCA AAU GGC ACA AUA CAU GAU AGA AUC CCU CAU	484
Leu Asp Asn Lys His Ser Asn Gly Thr Ile His Asp Arg Ile Pro His	
140 145 150 155	
CGA ACC CUA UUA AUG AAU GAG UUG GGU GUU CCA UUU CAU UUA GGA ACC	532
Arg Thr Leu Leu Met Asn Glu Leu Gly Val Pro Phe His Leu Gly Thr	
160 165 170	
AAA CAA GUG UGU GCA GCA UGG UCC AGC UCA AGU UGU CAC GAU GGA AAA	580
Lys Gln Val Cys Ala Ala Trp Ser Ser Ser Ser Cys His Asp Gly Lys	
175 180 185	

GCA Ala	UGG Trp	UUG Leu 190	CAU His	GUU Val	UGU Cys	GUC Val 195	ACA Thr	GGG Gly	GAU Asp	GAU Asp	AGA Arg	AAU Asn 200	GCA Ala	ACU Thr	GCU Ala	628
AGC Ser	UUC Phe 205	AUU Ile	UAU Tyr	GAC Asp	GGG Gly	AAG Lys 210	CUU Leu	GUG Val	GAC Asp	AGU Ser	AUU Ile 215	GGU Gly	UCA Ser	UGG Trp	UCU Ser	676
CAA Gln 220	AAU Asn	GUC Val	CUC Leu	AGG Arg	ACC Thr 225	CAG Gln	GAG Glu	UCG Ser	GAA Glu	UGC Cys 230	GUC Val	UGU Cys	AUC Ile	AAU Asn	GGG Gly 235	724
ACU Thr	UGC Cys	ACA Thr	GUA Val 240	GUA Val	AUG Met	ACU Thr	GAU Asp	GGA Gly	AGU Ser 245	GCA Ala	UCA Ser	GGA Gly	AGA Arg	GCU Ala 250	GAU Asp	772
ACU Thr	AGA Arg	AUA Ile 255	CUA Leu	UUC Phe	AUU Ile	AAA Lys	GAG Glu	GGG Gly 260	AAA Lys	AUU Ile	GUC Val	CAU His 265	AUU Ile	GGC Gly	CCA Pro	820
UUG Leu	UCA Ser	GGA Gly 270	AGU Ser	GCU Ala	CAG Gln	CAU His	GUA Val 275	GAG Glu	GAG Glu	UGU Cys	UCU Ser	UGU Cys 280	UAC Tyr	CCU Pro	CGA Arg	868
UAU Tyr 285	CCU Pro	GAC Asp	GUC Val	AGA Arg	UGU Cys	AUC Ile 290	UGC Cys	AGA Arg	GAC Asp	AAC Asn	UGG Trp 295	AAA Lys	GGC Gly	UCU Ser	AAU Asn	916
AGG Arg 300	CCC Pro	GUU Val	AUA Ile	GAC Asp	AUA Ile 305	AAU Asn	AUG Met	GAA Glu	GAU Asp	UAU Tyr 310	AGC Ser	AUU Ile	GAU Asp	UCC Ser	AGU Ser 315	964
UAU Tyr	GUG Val	UGC Cys	UCA Ser	GGG Gly 320	CUU Leu	GUU Val	GGC Gly	GAC Asp	ACA Thr 325	CCC Pro	AGG Arg	AAC Asn	GAC Asp	GAC Asp 330	AGC Ser	1012
UCU Ser	AGC Ser	AAU Asn 335	AGC Ser	AAU Asn	UGC Cys	AGG Arg	GAU Asp	CCU Pro 340	AAC Asn	AAU Asn	GAG Glu	AGA Arg	GGG Gly 345	AAU Asn	CCA Pro	1060
GGA Gly	GUG Val	AAA Lys 350	GGC Gly	UGG Trp	GCC Ala	UUU Phe	GAC Asp 355	AAU Asn	GGA Gly	GAU Asp	GAU Asp	GUA Val 360	UGG Trp	AUG Met	GGA Gly	1108
AGA Arg 365	ACA Thr	AUC Ile	AGC Ser	AAA Lys	GAU Asp	UUA Leu 370	CGC Arg	UCA Ser	GGU Gly	UAU Tyr	GAA Glu 375	ACU Thr	UUC Phe	AAA Lys	GUC Val	1156
AUU Ile 380	GGU Gly	GGU Gly	UGG Trp	UCC Ser	ACA Thr 385	CCU Pro	AAU Asn	UCC Ser	AAA Lys	UCG Ser 390	CAG Gln	GUC Val	AAU Asn	AGA Arg	CAG Gln 395	1204
GUC Val	AUA Ile	GUU Val	GAC Asp	AAC Asn 400	AAU Asn	AAU Asn	UGG Trp	UCU Ser	GGU Gly 405	UAC Tyr	UCU Ser	GGU Gly	AUU Ile	UUC Phe 410	UCU Ser	1252

GUU GAG GGC AAA AGC UGC AUC AAU AGG UGC UUU UAU GUG GAG UUG AUA 1300
Val Glu Gly Lys Ser Cys Ile Asn Arg Cys Phe Tyr Val Glu Leu Ile
415 420 425

AGG GGA AGG CCA CAG GAG ACU AGA GUA UGG UGG ACC UCA AAC AGU AUU 1348
Arg Gly Arg Pro Gln Glu Thr Arg Val Trp Trp Thr Ser Asn Ser Ile
430 435 440

GUU GUA UUU UGU GGC ACU UCA GGU ACU UAU GGA ACA GGC UCA UGG CCU 1396
Val Val Phe Cys Gly Thr Ser Gly Thr Tyr Gly Thr Gly Ser Trp Pro
445 450 455

GAU GGG GCG AAC AUC AAU UUC AUG CCU AUA UAACGUUUCG CAAUUUUAGA 1446
Asp Gly Ala Asn Ile Asn Phe Met Pro Ile
460 465

AAAAAACUCC UUGUUUCUAC U 1467

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 469 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Met Asn Pro Asn Gln Lys Thr Ile Thr Ile Gly Ser Val Ser Leu Thr
1 5 10 15

Ile Ala Thr Val Cys Phe Leu Met Gln Ile Ala Ile Leu Ala Thr Thr
20 25 30

Val Thr Leu His Leu Lys Gln His Glu Cys Asp Ser Pro Ala Ser Asn
35 40 45

Gln Val Met Pro Cys Glu Pro Ile Ile Ile Glu Arg Asn Ile Thr Glu
50 55 60

Ile Val Tyr Leu Asn Asn Thr Thr Ile Glu Lys Glu Ile Cys Pro Glu
65 70 75 80

Val Val Gly Tyr Arg Asn Trp Ser Lys Pro Gln Cys Gln Ile Thr Gly
85 90 95

Phe Ala Pro Phe Ser Lys Asp Asn Ser Ile Arg Leu Ser Ala Gly Gly

61

100					105					110					
Asp	Ile	Trp	Val	Thr	Arg	Glu	Pro	Tyr	Val	Ser	Cys	Asp	Pro	Gly	Lys
	115						120					125			
Cys	Tyr	Gln	Phe	Ala	Leu	Gly	Gln	Gly	Thr	Thr	Leu	Asp	Asn	Lys	His
	130					135					140				
Ser	Asn	Gly	Thr	Ile	His	Asp	Arg	Ile	Pro	His	Arg	Thr	Leu	Leu	Met
	145					150					155				160
Asn	Glu	Leu	Gly	Val	Pro	Phe	His	Leu	Gly	Thr	Lys	Gln	Val	Cys	Ala
				165					170					175	
Ala	Trp	Ser	Ser	Ser	Ser	Cys	His	Asp	Gly	Lys	Ala	Trp	Leu	His	Val
			180					185					190		
Cys	Val	Thr	Gly	Asp	Asp	Arg	Asn	Ala	Thr	Ala	Ser	Phe	Ile	Tyr	Asp
		195					200					205			
Gly	Lys	Leu	Val	Asp	Ser	Ile	Gly	Ser	Trp	Ser	Gln	Asn	Val	Leu	Arg
	210					215					220				
Thr	Gln	Glu	Ser	Glu	Cys	Val	Cys	Ile	Asn	Gly	Thr	Cys	Thr	Val	Val
	225					230					235				240
Met	Thr	Asp	Gly	Ser	Ala	Ser	Gly	Arg	Ala	Asp	Thr	Arg	Ile	Leu	Phe
				245					250					255	
Ile	Lys	Glu	Gly	Lys	Ile	Val	His	Ile	Gly	Pro	Leu	Ser	Gly	Ser	Ala
			260					265					270		
Gln	His	Val	Glu	Glu	Cys	Ser	Cys	Tyr	Pro	Arg	Tyr	Pro	Asp	Val	Arg
		275					280					285			
Cys	Ile	Cys	Arg	Asp	Asn	Trp	Lys	Gly	Ser	Asn	Arg	Pro	Val	Ile	Asp
	290					295					300				
Ile	Asn	Met	Glu	Asp	Tyr	Ser	Ile	Asp	Ser	Ser	Tyr	Val	Cys	Ser	Gly
	305					310					315				320
Leu	Val	Gly	Asp	Thr	Pro	Arg	Asn	Asp	Asp	Ser	Ser	Ser	Asn	Ser	Asn
				325					330					335	
Cys	Arg	Asp	Pro	Asn	Asn	Glu	Arg	Gly	Asn	Pro	Gly	Val	Lys	Gly	Trp
			340					345					350		
Ala	Phe	Asp	Asn	Gly	Asp	Asp	Val	Trp	Met	Gly	Arg	Thr	Ile	Ser	Lys
		355					360					365			
Asp	Leu	Arg	Ser	Gly	Tyr	Glu	Thr	Phe	Lys	Val	Ile	Gly	Gly	Trp	Ser
	370					375					380				
Thr	Pro	Asn	Ser	Lys	Ser	Gln	Val	Asn	Arg	Gln	Val	Ile	Val	Asp	Asn
	385					390					395				400

Asn Asn Trp Ser Gly Tyr Ser Gly Ile Phe Ser Val Glu Gly Lys Ser
405 410 415

Cys Ile Asn Arg Cys Phe Tyr Val Glu Leu Ile Arg Gly Arg Pro Gln
420 425 430

Glu Thr Arg Val Trp Trp Thr Ser Asn Ser Ile Val Val Phe Cys Gly
435 440 445

Thr Ser Gly Thr Tyr Gly Thr Gly Ser Trp Pro Asp Gly Ala Asn Ile
450 455 460

Asn Phe Met Pro Ile
465

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1566 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Influenza virus
- (B) STRAIN: wild type A/Ann Arbor/6/60 (H2N2) Egg Passage 2(3)

(vii) IMMEDIATE SOURCE:

- (B) CLONE: NP

(ix) FEATURE:

- (A) NAME/KEY: mutation
- (B) LOCATION: replace(113, "a")
- (D) OTHER INFORMATION: /note= "c in ca "master" strain; a in wt2(3); c in 1988 reported wild type E28-32 strain (manuscript) but a in 1988 reported wild type E28-32 strain

/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: conflict

(B) LOCATION: replace(146, "g")

(D) OTHER INFORMATION: /note= "g in ca "master" strain and in
wt2(3); a in 1988 reported wild type
E28-32 strain"
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: conflict

(B) LOCATION: replace(627, "c")

(D) OTHER INFORMATION: /note= "c in ca "master" strain and in
wt2(3); a in 1988 reported wild type
E28-32 strain"
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: conflict

(B) LOCATION: replace(909, "g")

(D) OTHER INFORMATION: /note= "g in ca "master" strain and in
wt2(3); c in 1988 reported wild type
E28-32 strain"
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: conflict

(B) LOCATION: replace(1550, "a")

(D) OTHER INFORMATION: /note= "a in ca "master" strain and in
wt2(3); deletion in 1988 reported wild
type E28-32 strain"
/citation= ([1][2])

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 46..1539

(D) OTHER INFORMATION: /product= "Nucleoprotein"
/gene= "NP"
/note= "nucleoprotein"
/citation= ([1][2])

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Herlocher, M L
Maassab, H F
Webster, R W

(B) TITLE: Molecular and biological changes in the cold adapted
master strain A/AA/6/60 (H2N2) influenza virus

(C) JOURNAL: Proceedings of the National Academy of Sciences of
the USA

(G) DATE: 1993

(K) RELEVANT RESIDUES IN SEQ ID NO:39: FROM 1 TO 1566

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Cox, N J
Kitame, F
Kendal, A P
Maassab, H F
Naeve, C

(B) TITLE: Identification of sequence changes in the cold-adapted
live attenuated influenza vaccine strain, A/Ann
Arbor/6/60 (H2N2)

(C) JOURNAL: Virology

(D) VOLUME: 167

(F) PAGES: 554-567

(G) DATE: 1988

(K) RELEVANT RESIDUES IN SEQ ID NO:39: FROM 1 TO 1566

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

AGCAAAAGCA GGGUAGAUAA UCACUCACUG AGUGACAUCA AAAUC AUG GCG UCC
Met Ala Ser

CAA	GGC	ACC	AAA	CGG	UCU	UAU	GAA	CAG	AUG	GAA	ACU	GAU	GGG	GAA	CGC	102
Gln	Gly	Thr	Lys	Arg	Ser	Tyr	Glu	Gln	Met	Glu	Thr	Asp	Gly	Glu	Arg	
	5					10					15					
CAG	AAU	GCA	AAU	GAA	AUC	AGA	GCA	UCC	GUC	GGG	AAG	AUG	AUU	GGU	GGA	150
Gln	Asn	Ala	Asn	Glu	Ile	Arg	Ala	Ser	Val	Gly	Lys	Met	Ile	Gly	Gly	
20					25					30					35	
AUU	GGA	CGA	UUC	UAC	AUC	CAA	AUG	UGC	ACC	GAA	CUU	AAA	CUC	AGU	GAU	198
Ile	Gly	Arg	Phe	Tyr	Ile	Gln	Met	Cys	Thr	Glu	Leu	Lys	Leu	Ser	Asp	
				40					45					50		
UAU	GAG	GGG	CGG	CUG	AUC	CAG	AAC	AGC	UUA	ACA	AUA	GAG	AGA	AUG	GUG	246
Tyr	Glu	Gly	Arg	Leu	Ile	Gln	Asn	Ser	Leu	Thr	Ile	Glu	Arg	Met	Val	
			55					60					65			
CUC	UCU	GCU	UUU	GAC	GAG	AGG	AGG	AAU	AAA	UAU	CUG	GAA	GAA	CAU	CCC	294
Leu	Ser	Ala	Phe	Asp	Glu	Arg	Arg	Asn	Lys	Tyr	Leu	Glu	Glu	His	Pro	
		70					75					80				
AGC	GCG	GGG	AAG	GAU	CCU	AAG	AAA	ACU	GGA	GGA	CCC	AUA	UAC	AAG	AGA	342
Ser	Ala	Gly	Lys	Asp	Pro	Lys	Lys	Thr	Gly	Gly	Pro	Ile	Tyr	Lys	Arg	
	85					90					95					
GUA	GAU	GGA	AAG	UGG	AUG	AGG	GAA	CUC	GUC	CUU	UAU	GAC	AAA	GAA	GAA	390
Val	Asp	Gly	Lys	Trp	Met	Arg	Glu	Leu	Val	Leu	Tyr	Asp	Lys	Glu	Glu	
100					105					110					115	
AUA	AGG	CGA	AUC	UGG	CGC	CAA	GCU	AAU	AAU	GGU	GAU	GAU	GCA	ACA	GCU	438
Ile	Arg	Arg	Ile	Trp	Arg	Gln	Ala	Asn	Asn	Gly	Asp	Asp	Ala	Thr	Ala	
				120					125					130		
GGU	CUG	ACU	CAC	AUG	AUG	AUC	UGG	CAU	UCC	AAU	UUG	AAU	GAU	ACA	ACA	486
Gly	Leu	Thr	His	Met	Met	Ile	Trp	His	Ser	Asn	Leu	Asn	Asp	Thr	Thr	
			135					140					145			
UAC	CAG	AGG	ACA	AGA	GCU	CUU	GUU	CGC	ACC	GGA	AUG	GAU	CCC	AGG	AUG	534
Tyr	Gln	Arg	Thr	Arg	Ala	Leu	Val	Arg	Thr	Gly	Met	Asp	Pro	Arg	Met	
		150					155					160				
UGC	UCU	UUG	AUG	CAG	GGU	UCG	ACU	CUC	CCU	AGG	AGG	UCU	GGA	GCC	GCA	582
Cys	Ser	Leu	Met	Gln	Gly	Ser	Thr	Leu	Pro	Arg	Arg	Ser	Gly	Ala	Ala	
	165					170					175					
GGC	GCU	GCA	GUC	AAA	GGA	GUU	GGG	ACA	AUG	GUG	AUG	GAG	UUG	AUC	AGG	630
Gly	Ala	Ala	Val	Lys	Gly	Val	Gly	Thr	Met	Val	Met	Glu	Leu	Ile	Arg	
180					185					190					195	
AUG	AUC	AAA	CGU	GGG	AUC	AAU	GAU	CGG	AAC	UUC	UGG	AGA	GGU	GAG	AAU	678
Met	Ile	Lys	Arg	Gly	Ile	Asn	Asp	Arg	Asn	Phe	Trp	Arg	Gly	Glu	Asn	
				200					205					210		
GGG	CGG	AAA	ACA	AGG	AAU	GCU	UAU	GAG	AGA	AUG	UGC	AAC	AUU	CUC	AAA	726
Gly	Arg	Lys	Thr	Arg	Asn	Ala	Tyr	Glu	Arg	Met	Cys	Asn	Ile	Leu	Lys	
			215					220					225			

GGA	AAA	UUU	CAA	ACA	GCU	GCA	CAA	AGA	GCA	AUG	AUG	GAU	CAA	GUG	AGA	774
Gly	Lys	Phe	Gln	Thr	Ala	Ala	Gln	Arg	Ala	Met	Met	Asp	Gln	Val	Arg	
		230					235					240				
GAA	AGC	CGG	AAC	CCA	GGA	AAU	GCU	GAG	AUC	GAA	GAU	CUC	AUC	UUU	CUG	822
Glu	Ser	Arg	Asn	Pro	Gly	Asn	Ala	Glu	Ile	Glu	Asp	Leu	Ile	Phe	Leu	
	245					250					255					
GCA	CGG	UCU	GCA	CUC	AUA	UUG	AGA	GGG	UCA	GUU	GCU	CAC	AAA	UCU	UGU	870
Ala	Arg	Ser	Ala	Leu	Ile	Leu	Arg	Gly	Ser	Val	Ala	His	Lys	Ser	Cys	
260					265					270					275	
CUG	CCU	GCC	UGU	GUG	UAU	GGA	CCU	GCC	GUA	GCC	AGU	GGG	UAC	GAC	UUC	918
Leu	Pro	Ala	Cys	Val	Tyr	Gly	Pro	Ala	Val	Ala	Ser	Gly	Tyr	Asp	Phe	
				280					285					290		
GAA	AAA	GAG	GGA	UAC	UCU	UUA	GUA	GGG	AUA	GAC	CCU	UUC	AAA	CUG	CUU	966
Glu	Lys	Glu	Gly	Tyr	Ser	Leu	Val	Gly	Ile	Asp	Pro	Phe	Lys	Leu	Leu	
			295					300					305			
CAA	AAC	AGC	CAA	GUA	UAC	AGC	CUA	AUC	AGA	CCG	AAU	GAG	AAU	CCA	GCA	1014
Gln	Asn	Ser	Gln	Val	Tyr	Ser	Leu	Ile	Arg	Pro	Asn	Glu	Asn	Pro	Ala	
		310					315					320				
CAC	AAG	AGU	CAG	CUG	GUG	UGG	AUG	GCA	UGC	AAU	UCU	GCU	GCA	UUU	GAA	1062
His	Lys	Ser	Gln	Leu	Val	Trp	Met	Ala	Cys	Asn	Ser	Ala	Ala	Phe	Glu	
	325					330					335					
GAU	CUA	AGA	GUA	UCA	AGC	UUC	AUC	AGA	GGG	ACC	AAA	GUA	AUC	CCA	AGG	1110
Asp	Leu	Arg	Val	Ser	Ser	Phe	Ile	Arg	Gly	Thr	Lys	Val	Ile	Pro	Arg	
340					345					350					355	
GGG	AAA	CUU	UCC	ACU	AGA	GGA	GUA	CAA	AUU	GCU	UCA	AAU	GAA	AAC	AUG	1158
Gly	Lys	Leu	Ser	Thr	Arg	Gly	Val	Gln	Ile	Ala	Ser	Asn	Glu	Asn	Met	
				360					365					370		
GAU	ACU	AUG	GGA	UCA	AGU	ACU	CUU	GAA	CUG	AGA	AGC	AGG	UAC	UGG	GCC	1206
Asp	Thr	Met	Gly	Ser	Ser	Thr	Leu	Glu	Leu	Arg	Ser	Arg	Tyr	Trp	Ala	
			375					380					385			
AUA	AGG	ACC	AGA	AGU	GGA	GGA	AAC	ACU	AAU	CAA	CAG	AGG	GCC	UCU	GCA	1254
Ile	Arg	Thr	Arg	Ser	Gly	Gly	Asn	Thr	Asn	Gln	Gln	Arg	Ala	Ser	Ala	
		390					395					400				
GGU	CAA	AUC	AGU	GUA	CAA	CCU	ACG	UUU	UCU	GUG	CAA	AGA	AAC	CUC	CCA	1302
Gly	Gln	Ile	Ser	Val	Gln	Pro	Thr	Phe	Ser	Val	Gln	Arg	Asn	Leu	Pro	
	405					410					415					
UUU	GAC	AAA	CCA	ACC	AUC	AUG	GCA	GCA	UUC	ACU	GGG	AAU	GCA	GAG	GGA	1350
Phe	Asp	Lys	Pro	Thr	Ile	Met	Ala	Ala	Phe	Thr	Gly	Asn	Ala	Glu	Gly	
420					425					430					435	
AGA	ACA	UCA	GAC	AUG	AGG	GCA	GAA	AUC	AUA	AGG	AUG	AUG	GAA	GGU	GCA	1398
Arg	Thr	Ser	Asp	Met	Arg	Ala	Glu	Ile	Ile	Arg	Met	Met	Glu	Gly	Ala	
				440					445					450		

AAA CCA GAA GAA GUG UCC UUC CAG GGG CGG GGA GUC UUC GAG CUC UCG	1446
Lys Pro Glu Glu Val Ser Phe Gln Gly Arg Gly Val Phe Glu Leu Ser	
455 460 465	
GAC GAA AAG GCA ACG AAC CCG AUC GUG CCC UCU UUU GAC AUG AGU AAU	1494
Asp Glu Lys Ala Thr Asn Pro Ile Val Pro Ser Phe Asp Met Ser Asn	
470 475 480	
GAA GGA UCU UAU UUC UUC GGA GAC AAU GCA GAG GAG UAC GAC AAU	1539
Glu Gly Ser Tyr Phe Phe Gly Asp Asn Ala Glu Glu Tyr Asp Asn	
485 490 495	
UAAGGAAAAA AUACCCUUGU UUCUACU	1566

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 498 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Met	Ala	Ser	Gln	Gly	Thr	Lys	Arg	Ser	Tyr	Glu	Gln	Met	Glu	Thr	Asp
1				5					10					15	
Gly	Glu	Arg	Gln	Asn	Ala	Asn	Glu	Ile	Arg	Ala	Ser	Val	Gly	Lys	Met
			20					25					30		
Ile	Gly	Gly	Ile	Gly	Arg	Phe	Tyr	Ile	Gln	Met	Cys	Thr	Glu	Leu	Lys
		35					40					45			
Leu	Ser	Asp	Tyr	Glu	Gly	Arg	Leu	Ile	Gln	Asn	Ser	Leu	Thr	Ile	Glu
	50					55					60				
Arg	Met	Val	Leu	Ser	Ala	Phe	Asp	Glu	Arg	Arg	Asn	Lys	Tyr	Leu	Glu
65					70				75					80	
Glu	His	Pro	Ser	Ala	Gly	Lys	Asp	Pro	Lys	Lys	Thr	Gly	Gly	Pro	Ile
				85					90					95	
Tyr	Lys	Arg	Val	Asp	Gly	Lys	Trp	Met	Arg	Glu	Leu	Val	Leu	Tyr	Asp
			100					105					110		
Lys	Glu	Glu	Ile	Arg	Arg	Ile	Trp	Arg	Gln	Ala	Asn	Asn	Gly	Asp	Asp
		115					120					125			

Ala Thr Ala Gly Leu Thr His Met Met Ile Trp His Ser Asn Leu Asn
130 135 140

Asp Thr Thr Tyr Gln Arg Thr Arg Ala Leu Val Arg Thr Gly Met Asp
145 150 155 160

Pro Arg Met Cys Ser Leu Met Gln Gly Ser Thr Leu Pro Arg Arg Ser
165 170 175

Gly Ala Ala Gly Ala Ala Val Lys Gly Val Gly Thr Met Val Met Glu
180 185 190

Leu Ile Arg Met Ile Lys Arg Gly Ile Asn Asp Arg Asn Phe Trp Arg
195 200 205

Gly Glu Asn Gly Arg Lys Thr Arg Asn Ala Tyr Glu Arg Met Cys Asn
210 215 220

Ile Leu Lys Gly Lys Phe Gln Thr Ala Ala Gln Arg Ala Met Met Asp
225 230 235 240

Gln Val Arg Glu Ser Arg Asn Pro Gly Asn Ala Glu Ile Glu Asp Leu
245 250 255

Ile Phe Leu Ala Arg Ser Ala Leu Ile Leu Arg Gly Ser Val Ala His
260 265 270

Lys Ser Cys Leu Pro Ala Cys Val Tyr Gly Pro Ala Val Ala Ser Gly
275 280 285

Tyr Asp Phe Glu Lys Glu Gly Tyr Ser Leu Val Gly Ile Asp Pro Phe
290 295 300

Lys Leu Leu Gln Asn Ser Gln Val Tyr Ser Leu Ile Arg Pro Asn Glu
305 310 315 320

Asn Pro Ala His Lys Ser Gln Leu Val Trp Met Ala Cys Asn Ser Ala
325 330 335

Ala Phe Glu Asp Leu Arg Val Ser Ser Phe Ile Arg Gly Thr Lys Val
340 345 350

Ile Pro Arg Gly Lys Leu Ser Thr Arg Gly Val Gln Ile Ala Ser Asn
355 360 365

Glu Asn Met Asp Thr Met Gly Ser Ser Thr Leu Glu Leu Arg Ser Arg
370 375 380

Tyr Trp Ala Ile Arg Thr Arg Ser Gly Gly Asn Thr Asn Gln Gln Arg
385 390 395 400

Ala Ser Ala Gly Gln Ile Ser Val Gln Pro Thr Phe Ser Val Gln Arg
405 410 415

Asn Leu Pro Phe Asp Lys Pro Thr Ile Met Ala Ala Phe Thr Gly Asn

420

425

430

Ala Glu Gly Arg Thr Ser Asp Met Arg Ala Glu Ile Ile Arg Met Met
435 440 445

Glu Gly Ala Lys Pro Glu Glu Val Ser Phe Gln Gly Arg Gly Val Phe
450 455 460

Glu Leu Ser Asp Glu Lys Ala Thr Asn Pro Ile Val Pro Ser Phe Asp
465 470 475 480

Met Ser Asn Glu Gly Ser Tyr Phe Phe Gly Asp Asn Ala Glu Glu Tyr
485 490 495

Asp Asn